? t s2/7/all

2/7/1 (Item 1 from file: 5)
DIALOG(R)File 5:BIOSIS PREVIEWS(R)
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12146840 BIOSIS NO.: 199900441689
Advances in the understanding of aluminum toxicity and the develcpment of aluminum-tolerant **transgenic plants**.
BOOK TITLE: Advances in Agronomy
AUTHOR: De la Fuente-Martinez Juan Manuel(a); Herrera-Estrella Luis
BOOK AUTHOR/EDITOR: Sparks D L: Ed
AUTHOR ADDRESS: (a)Centro de Biotechnolgia, ITESM CEDES 6 piso, Guanajuato **Mexico
JOURNAL: Advances in Agronomy 66p103-120 1999
BOOK PUBLISHER: Academic Press, Inc., 1250 Sixth Ave., San Diego, California 92101, USA
Academic Press Ltd., 14 Belgrave Square, 24-28 Oval Road, London NW1 70X, England, UK
ISSN: 0065-2113 ISBN: 0-12-000766-5
DOCUMENT TYPE: Book; Literature Review
RECORD TYPE: Citation
LANGUAGE: English

2/7/2 (Item 2 from file: 5)
DIALOG(R)File 5:BIOSIS PREVIEWS(R)
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12044037 BIOSIS NO.: 199900324556
Over expression of mitochondrial **citrate synthase** gene improves the growth of carrot cells in Al-phosphate medium.
AUTHOR: Koyama Hiroyuki(a); Takita Eiji; Kawamura Ayako; Hara Tetsuo; Shibata Daisuke
AUTHOR ADDRESS: (a)Laboratory of Plant Cell Technology, Faculty of Agriculture, Gifu University, 1-1 Yanagido, Gifu**Japan
JOURNAL: Plant and Cell Physiology 40 (5):p482-488 May, 1999
ISSN: 0032-0781
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English

ABSTRACT: A mitochondrial **citrate synthase** (CS) of Arabidopsis thaliana was introduced into carrot (Daucus carota L. cv. MS Yonsun) cells by Agrobacterium tumefaciens-mediated **transformation**. **Transgenic** cell lines had high CS activity, the highest value observed was 0.24 mumol (mg protein)-1 min-1 which was 1.9-fold of that in wild-type cells. Transcript levels of DcCS were similar between **transgenic** lines, but those of AtCS were increased as the CS activity of cells was increased. Isoelectric focussing revealed that the CS polypeptide of the **transgenic** lines had a pI value different from that of the wild-type cells, although the molecular mass was the same. These results indicate that the CS polypeptides of A. thaliana were expressed and processed to the mature form in carrot cells. The growth rate and excretion was 2.2-2.8 and 2.8-4.0 fold greater in the **transgenic** cells than in the wild type cells, respectively. Phosphate uptake from Al-phosphate also increased in **transgenic**

cells. It appeares, the overexpression of mitochondrial **citrate synthase** in carrot cells improves the growth rate in Al-phosphate medium possibly as a result of increased **citrate** excretion.

2/7/3 (Item 3 from file: 5)
DIALOG(R)File 5:BIOSIS PREVIEWS(R)
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11042826 BIOSIS NO.: 199900323345
Oligomeric proteins containing N-terminal targeting signals are imported into peroxisomes in **transgenic** Arabidopsis.
AUTHOR: Kato Akira; Hayashi Makoto; Nishimura Mikio(a)
AUTHOR ADDRESS: (a)Department of Cell Biology, National Institute for Basic Biology, Okazaki, 444-8585**Japan
JOURNAL: Plant and Cell Physiology 40 (6):p586-591 June, 1999
ISSN: 0032-0781
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English

ABSTRACT: Employing **transgenic** Arabidopsis **plants**, we analyzed the mechanism for the translocation of peroxisomal proteins from the cytosol into the matrix that is mediated by the N-terminal targeting signal. A hybrid Arabidopsis variety was generated which accumulates two kinds of originally bacterial proteins, beta-glucuronidase (GUS) and a GUS chimeric protein designated as CS-DELTAC42-GUS, that carries the N-terminal targeting signal for glyoxysomal **citrate synthase**. Because the CS-DELTAC42-GUS is targeted to peroxisomes but had never been observed to be processed to produce the mature protein, it can be distinguished from the GUS protein by its molecular size. Cell fractionation analyses showed that the native GUS protein, although lacking the targeting signal, was co-localized with the CS-DELTAC42-GUS protein in the peroxisomes of the hybrid **plant**. It is suggested that the native GUS protein forms oligomeric structures with the peroxisome-targeted chimeric proteins and can therefore be transportedinto peroxisomes. Sucrose density gradient centrifugation revealed that the native GUS and the chimeric GUS indeed are present both as a dimer and a tetramer in the Arabidopsis hybrid variety.

2/7/4 (Item 4 from file: 5)
DIALOG(R)File 5:BIOSIS PREVIEWS(R)
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11997240 BIOSIS NO.: 199900203349
Chloroplast Cpn20 forms a tetrameric structure in Arabidopsis thaliana.
AUTHOR: Koumoto Yasuko; Shimada Tomoo; Kondo Maki; Takao Toshifumi; Shimonishi Yasutsugu; Hara-Nishimura Ikuko; Nishimura Mikio(a)
AUTHOR ADDRESS: (a)Department of Cell Biology, National Institute for Basic Biology, 38 Nishigonaka, Myodaiji, Okaz**Japan
JOURNAL: Plant Journal 17 (5):p467-477 March, 1999
ISSN: 0960-7412
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English

ABSTRACT: Chloroplast chaperonin 20 (Cpn20) in higher **plants** is a functional homologue of the Escherichia coli GroES, which is a critical regulator of chaperonin-mediated protein folding. The cDNA for a Cpn20 homologue of Arabidopsis thaliana was isolated. It was 958 bp long, encoding a protein of 253 amino acids. The protein was composed of an N-terminal chloroplast transit peptide, and the predicted mature region comprised two distinct GroES domains that showed 42% amino acid identity

to each other. The isolated cDNA was constitutively expressed in **transgenic** tobacco. Immunogold labelling showed that Cpn20 is accumulated in chloroplasts of **transgenic** tobacco. A Northern blot analysis revealed that mRNA for the chloroplast Cpn20 is abundant in leaves and is increased by heat treatment. To examine the oligomeric structure of Cpn20, a histidine-tagged construct lacking the transit peptide was expressed in E. coli and purified by affinity chromatography. Gel-filtration and cross-linking analyses showed that the expressed products formed a tetramer. The expressed products could substitute for GroES to assist the refolding of **citrate synthase** under non-permissive conditions. The analysis on the subunit stoichiometry of the GroEL-Cpn20 complex also revealed that the functional complex is composed of a GroEL tetradecamer and a Cpn20 tetramer.

2/7/5 (Item 5 from file: 5)
DIALOG(R)File 5:BIOSIS PREVIEWS(R)
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11990168 BIOSIS NO.: 199800171500
Glyoxysomal malate dehydrogenase in pumpkin: Cloning of a cDNA and functional analysis of its presequence.
AUTHOR: Kato Akira; Takeda-Yoshikawa Yoko; Hayashi Makoto; Kondo Maki; Hara-Nishimura Ikuko; Nishimura Mikio(a)
AUTHOR ADDRESS: (a)Dep. Cell Biol., Natl. Inst. Basic Biol., Okazaki 444** Japan
JOURNAL: Plant and Cell Physiology 39 (2):p186-195 Feb., 1998
ISSN: 0032-0781
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Glyoxysomal malate dehydrogenase (gMDH) is an enzyme of the glyoxylate cycle that participates in degradation of storage oil. We have cloned a cDNA for gMDH from etiolated pumpkin cotyledons that encodes a polypeptide consisting of 356 amino acid residues. The nucleotide and N-terminal amino acid sequences revealed that gMDH is synthesized as a precursor with an N-terminal extrapeptide. The N-terminal presequence of 36 amino acid residues contains two regions homologous to those of other microbody proteins, which are also synthesized as large precursors. To investigate the functions of the N-terminal presequence of gMDH, we generated **transgenic** Arabidopsis that expressed a chimeric protein consisting of beta-glucuronidase and the N-terminal region of gMDH. Immunological and immunocytochemical studies revealed that the chimeric protein was imported into microbodies such as glyoxysomes and leaf peroxisomes and was then subsequently processed. Site-directed mutagenesis studies showed that the conserved amino acids in the N-terminal presequence, Arg-10 and His-17, function as recognition sites for the targeting to **plant** microbodies, and Cys-36 in the presequence is responsible for its processing. These results correspond to those from the analyses of glyoxysomal **citrate synthase** (gCS), which was also synthesized as a large precursor, suggesting that common mechanisms that can recognize the targeting or the processing of gMDH and gCS function in higher **plant** cells.

2/7/6 (Item 6 from file: 5)
DIALOG(R)File 5:BIOSIS PREVIEWS(R)
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11759618 BIOSIS NO.: 199799680763
Protein import to microbodies in **transgenic** Arabidopsis.
AUTHOR: Kato Akira(a); Hayashi Makoto(a); Kondo Maki; Nishimura Mikio(a)
AUTHOR ADDRESS: (a)Dep. Cell Biol., Natl. Inst. Basic Biol., Okazaki 444** Japan
JOURNAL: Plant Physiology (Rockville) 114 (3 SUPPL.):p234 1997

CONFERENCE/MEETING: PLANT BIOLOGY '97: 1997 Annual Meetings of the American Society of Plant Physiologists and the Canadian Society of Plant Physiologists, Japanese Society of Plant Physiologists and the Australian Society of Plant Physiologists Vancouver, British Columbia, Canada August 2-6, 1997
ISSN: 0032-0889
RECORD TYPE: Citation
LANGUAGE: English

2/7/7 (Item 7 from file: 5)
DIALOG(R)File 5:BIOSIS PREVIEWS(R)
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10950312 BIOSIS NO.: 199799571457
Nitrate acts as a singal to induce organic acid metabolism and repress starch metabolism in tobacco.
AUTHOR: Scheible Wolf-Ruediger; Gonzalez-Fontes Agustin; Lauerer Marianne; Mueller-Roeber Bernd; Caboche Michel; Stitt Mark(a)
AUTHOR ADDRESS: (a)Bot. Inst., Univ. Heidelberg, Im Neuenheimer Feld 360, 69120 Heidelberg**Germany
JOURNAL: Plant Cell 9 (5):p783-798 1997
ISSN: 1040-4651
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Nia30(145) **transformants** with very low nitrate reductase activity provide an in vivo screen to identify processes that are regulated by nitrate. Nia30(145) resembles nitrate-limited wild-type **plants** with respect to growth rate and protein and amino acid content but accumulates large amounts of nitrate when it is grown on high nitrate. The transcripts for nitrate reductase (NR), nitrite reductase, cytosolic glutamine **synthetase**, and glutamate **synthase** increased; NR and nitrite reductase activity increased in leaves and roots; and glutamine **synthetase** activity increased in roots. The transcripts for phosphoenolpyruvate carboxylase, cytosolic pyruvate kinase, **citrate synthase**, and NADP-isocitrate dehydrogenase increased; phosphoenolpyruvate carboxylase activity increased; and malate, **citrate**, isocitrate, and alpha-oxoglutarate accumulated in leaves and roots. There was a decrease of the ADP-glucose pyrophosphorylase transcript and activity, and starch decreased in the leaves and roots. After adding 12 mM nitrate to nitrate-limited Nia30(145), the transcripts for NR and phosphoenolpyruvate carboxylase increased, and the transcripts for ADP-glucose pyrophosphorylase decreased within 2 and 4 hr, respectively. Starch was remobilized at almost the same rate as in wild-type **plants**, even though growth was not stimulated in Nia30(145). It is proposed that nitrate acts as a signal to initiate coordinated changes in carbon and nitrogen metabolism.

2/7/8 (Item 8 from file: 5)
DIALOG(R)File 5:BIOSIS PREVIEWS(R)
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10610179 BIOSIS NO.: 199699231324
Targeting and processing of a chimeric protein with the N-terminal presequence of the precursor to glyoxysomal **citrate synthase**.

AUTHOR: Kato Akira; Hayashi Makoto; Kondo Maki; Nishimura Mikio(a)
AUTHOR ADDRESS: (a)Dep. Cell Biol., Natl. Inst. Basic Biol., Okazaki 444** Japan
JOURNAL: Plant Cell 8 (9):p1601-1611 1996
ISSN: 1040-4651
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Glyoxysomal **citrate synthase** in pumpkin is synthesized as a precursor that has a cleavable presequence at its N-terminal end. To investigate the role of the presequence in the transport of the protein to the microbodies, we generated **transgenic** Arabidopsis **plants** that expressed beta-glucuronidase with the N-terminal presequence of the precursor to the glyoxysomal **citrate synthase** of pumpkin. Immunogold labeling and cell fractionation studies showed that the chimeric protein was transported into microbodies and subsequently was processed. The chimeric protein was transported to functionally different microbodies, such as glyoxysomes, leaf peroxisomes, and unspecialized microbodies. These observations indicated that the transport of glyoxysomal **citrate synthase** is mediated by its N-terminal presequence and that the transport system is functional in all **plant** microbodies. Site-directed mutagenesis of the conserved amino acids in the presequence caused abnormal targeting and inhibition of processing of the chimeric protein, suggesting that the conserved amino acids in the presequence are required for recognition of the target or processing.

2/7/9 (Item 9 from file: 5)
DIALOG(R)File 5:BIOSIS PREVIEWS(R)
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10295223 BIOSIS NO.: 199698750141
Effects of electron transport inhibitors and some metabolites on 6-14C-**citrate transformation** in **plants**.
AUTHOR: Popova T N(a); Igamberdiev A U; Velichko Yu I
AUTHOR ADDRESS: (a)Dep. Plant Physiol. Biochem., Fac. Biol. Soil Sci., Voronezh State Univ., Universitetskaya pl. 1**Russia
JOURNAL: Fiziologiya Rastenii (Moscow) 42 (5):p765-772 1995
ISSN: 0015-3303
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: Russian; Non-English
SUMMARY LANGUAGE: Russian; Non-English

ABSTRACT: The effects of some electron transport chain (ETC) inhibitors and some tricarboxylic acid cycle (TCC) metabolites, photorespiratory pathways, and ascorbate-oxidase system on 6-c-14-**citrate** metabolization were studied in maize Zea mays and wheat Triticum aestivum leaves. Carbon-14 dioxide excretion was inhibited by potassium cyanide and salicylhydroxamate; rotenone stimulated decarboxylation. The metabolization was carried out through isocitrate dehydrogenase (IDH) reaction. Ascorbate stimulated 6-C-14-**citrate** oxidation in the presence of glutathione. This phenomenon is associated with enzyme activation and conjugation of its function with NADH-oxidasing ascorbate oxidase system. The metabolization of 6-C-14-**citrate** was inhibited in the presence of succinate and glyoxylate apparently, in connection with isocitrate synthesis intensification in **synthase** reaction of extraglyoxysomal isocitrate lyase. The inhibition of cyanide-sensitive and cyanide-resistant electron transport apparently resulted in the intensification of **citrate** utilization through the reaction of GABA-breakdown of TCC. It was concluded that the intermediates of TCC and photorespiratory processes can play an important role in the regulation of **citrate transformation** pathway. **Citrate** metabolism conjugation with the most important cellular processes and various ETC made it possible to regulate metabolic **transformations** of **citrate** as a function of the needs of a **plant** organism.

2/7/10 (Item 10 from file: 5)
DIALOG(R)File 5:BIOSIS PREVIEWS(R)
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09748883 BIOSIS NO.: 199598203801
Structure and molecular chaperone activity of small heat shock proteins.
AUTHOR: Lee Garrett; Osteryoung Katherine; Suzuki Teri; Wehmeyer Nadja; Krawitz Denise; Vierling Elizabeth
AUTHOR ADDRESS: Dep. Biochem., Univ. Ariz., Tucson, AZ 85721**USA
JOURNAL: Journal of Cellular Biochemistry Supplement 0 (19A):p128 1995
CONFERENCE/MEETING: Keystone Symposium on Plant Cell Biology: Mechanisms, Molecular Machinery, Signals and Pathways Taos, New Mexico, USA January 7-13, 1995
ISSN: 0733-1959
RECORD TYPE: Citation
LANGUAGE: English

2/7/11 (Item 11 from file: 5)
DIALOG(R)File 5:BIOSIS PREVIEWS(R)

09738770 BIOSIS NO.: 199598193688
Correction of PREVIEWS 97551017. Metabolic studies on Saccharomyces cerevisiae containing fused **citrate synthase**/malate dehydrogenase. Addition of author name. Erratum published in BIOCHEMISTRY Vol. 33. Iss. 49. 1994. p. 14948.
AUTHOR: Lindbladh Christer; Brodeur Richard D; Small William C; Lilius G; Bulow Leif; Mosbach Klaus; Srere Paul A(a)
AUTHOR ADDRESS: (a)Pre-Clin. Sci. Unit, Dep. Veterans Aff. Med. Cent., 4500 S. Lancaster Rd., Dallas, TX 75216**USA
JOURNAL: Biochemistry 33 (39):p11684-11691 1994
ISSN: 0006-2960
DOCUMENT TYPE: Article; Erratum
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: We have constructed two different fusion proteins consisting of the C-terminal end of CS1 fused in-frame to the N-terminal end of MDH1 and HSA, respectively. The fusion proteins were expressed in mutants of Saccharomyces cerevisiae in which CS1 and MDH1 had been deleted and the phenotypes of the **transformants** characterized. The results show that the fusion proteins are transported into the mitochondria and that they restore the ability for the yeast mutants CS1-, MDH1-, and CS1-/MDH1- to grow on acetate. Determination of CS1 activity in isolated mitochondria showed a 10-fold increase for the strain that expressed native CS1, relative to the parental. In the **transformant** with CS1/MDH1 fusion protein, parental levels of CS1 were observed, while one-fifth this amount was observed for the strain expressing the CS1/HSA conjugate. Oxygen consumption studies on isolated mitochondria did not show any significant differences between parental-type yeast and the strains expressing the different fusion proteins or native CS1. (3-13C)Propionate was used to study the Krebs TCA cycle metabolism of yeast cells containing CS1/MDH1 fusion constructs. The 13C NMR study was performed in respiratory-competent parental yeast cells and using the genetically engineered yeast cells consisting of CS1- mutants expressing native CS1 and the fusion proteins CS1/MDH1 and CS1/HSA, respectively. (3-13C)Propionate is believed to be metabolized to (2-13C)succinyl-CoA before it enters the TCA cycle in the mitochondria. This metabolite is then oxidized through two symmetrical intermediates, succinate and fumarate, followed by conversion to malate, oxalacetate, and other metabolites such as alanine. If the symmetrical intermediates randomly diffuse between the enzymes in the mitochondria, the 13C label should be equally distributed on the C2 and C3 positions of malate and alanine. However, if succinate and fumarate are directly transferred with conserved orientation between the active sites of the enzymes succinate thiokinase, succinate dehydrogenase, and fumarase, the labeling of the C2 and C3 positions of malate, oxalacetate, and alanine will be asymmetrical. During oxidation of (3-13C)propionate in parental cells, we observed an asymmetric labeling of the C2 and C3 positions of alanine

where the 13C enrichment was significantly higher in the C3 position (C3/C2 = 14.3). Inhibition of succinate dehydrogenase with increasing amounts of malonate resulted in a concentration-dependent decrease in the asymmetric labeling of alanine. When (3-13C)propionate oxidation was performed in the CS1- yeast cells containing CS1, CS1/MDH1, and CS1/HSA, the CS/HSA **transformant** displayed significantly decreased asymmetry in the labeling of the C2 and C3 positions of alanine (C3/C2 = 2.9). No significant difference was found between parental cells and the CS1 and CS1/MDH1 **transformants**. Growth experiments on rich medium did not show any differences between the **transformants**. On minimal medium, however, the CS1/HSA **transformant** displayed an increased doubling time. These data show that, in yeast cells containing the CS1/MDH1 fusion protein, symmetrical intermediates are transferred directly from TCA cycle enzyme to TCA cycle enzyme under in vivo conditions just as is observed in the parental cell. The data also show that it is possible to alter this effect in the TCA cycle pathway by introduction of a genetically engineered CS1/HSA fusion protein. We also discuss these data in the context of the metabolon hypothesis for the Krebs TCA cycle.

2/7/12 (Item 12 from file: 5)
DIALOG(R)File 5:BIOSIS PREVIEWS(R)

09738648 BIOSIS NO.: 199598193566
Inhibition of flower formation by antisense repression of mitochondrial **citrate synthase** in **transgenic** potato **plants** leads to a specific disintegration of the ovary tissues of flowers.
AUTHOR: Landschuetze Volker; Willmitzer Lothar; Mueller-Roeber Bernd
AUTHOR ADDRESS: Inst. Genbiol. Forschung Berlin GmbH, Ihnestrasse 63, 14195 Berlin**Germany
JOURNAL: EMBO (European Molecular Biology Organization) Journal 14 (4):p 660-666 1995
ISSN: 0261-4189
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The tricarboxylic acid (TCA) cycle constitutes a major component of the mitochondrial metabolism of eucaryotes, including higher **plants**. To analyze the importance of this pathway, we down-regulated mitochondrial **citrate synthase** (mCS; EC 4.1.3.7), the first enzyme of the TCA cycle, in **transgenic** potato **plants** using an antisense RNA approach. Several **transformants** were identified with reduced **citrate synthase** activity (down to apprx 6% of wild-type activity). These **plants** were indistinguishable from wild-type **plants** in the greenhouse during vegetative growth. A major change, however, was seen upon initiation of the generative phase (flower formation). In the case of **transgenic** **plants** with a strong reduction in **citrate synthase** activity (lt 30% of wild-type levels), flower buds formed gt 2 weeks later as compared with wild-type **plants**. Furthermore, flower buds from these **plants** did not develop into mature flowers but rather were aborted at an early stage of development. Microscopic analysis showed that in these cases ovaries disintegrated during flower development. We conclude that the TCA cycle is of major importance during the transition from the vegetative to the generative phase.

2/7/13 (Item 13 from file: 5)
DIALOG(R)File 5:BIOSIS PREVIEWS(R)

09542647 BIOSIS NO.: 199497551017
Metabolic studies on Saccharomyces cerevisiae containing fused **citrate synthase**/malate dehydrogenase.

AUTHOR: Lindbladh Christer; Brodeur Richard D; Lilius G; Bulow Leif; Mosbach Klaus; Srere Paul A(a)
AUTHOR ADDRESS: (a)Pre-Clin. Sci. Unit, Dep. Veterans Aff. Med. Cent., 4500 S. Lancaster Rd., Dallas, TX 75216**USA
JOURNAL: Biochemistry 33 (39):p11684-11691 1994
ISSN: 0006-2960
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: We have constructed two different fusion proteins consisting of the C-terminal end of CS1 fused in-frame to the N-terminal end of MDH1 and HSA, respectively. The fusion proteins were expressed in mutants of Saccharomyces cerevisiae in which CS1 and MDH1 had been deleted and the phenotypes of the **transformants** characterized. The results show that the fusion proteins are transported into the mitochondria and that they restore the ability for the yeast mutants CS1-, MDH1-, and CS1-/MDH1- to grow on acetate. Determination of CS1 activity in isolated mitochondria showed a 10-fold increase for the strain that expressed native CS1, relative to the parental. In the **transformant** with CS1/MDH1 fusion protein, parental levels of CS1 were observed, while one-fifth this amount was observed for the strain expressing the CS1/HSA conjugate. Oxygen consumption studies on isolated mitochondria did not show any significant differences between parental-type yeast and the strains expressing the different fusion proteins or native CS1. (3-13C)Propionate was used to study the Krebs TCA cycle metabolism of yeast cells containing CS1/MDH1 fusion constructs. The 13C NMR study was performed in respiratory-competent parental yeast cells and using the genetically engineered yeast cells consisting of CS1- mutants expressing native CS1 and the fusion proteins CS1/MDH1 and CS1/HSA, respectively. (3-13C)Propionate is believed to be metabolized to (2-13C)succinyl-CoA before it enters the TCA cycle in the mitochondria. This metabolite is then oxidized through two symmetrical intermediates, succinate and fumarate, followed by conversion to malate, oxalacetate, and other metabolites such as alanine. If the symmetrical intermediates randomly diffuse between the enzymes in the mitochondria, the 13C label should be equally distributed on the C2 and C3 positions of malate and alanine. However, if succinate and fumarate are directly transferred with conserved orientation between the active sites of the enzymes succinate thiokinase, succinate dehydrogenase, and fumarase, the labeling of the C2 and C3 positions of malate, oxalacetate, and alanine will be a symmetrical. During oxidation of (3-13C) propionate in parental cells, we observed an asymmetric labeling of the C2 and C3 positions of alanine where the 13C enrichment was significantly higher in the C3 position (C3/C2 = 14.3). Inhibition of succinate dehydrogenase with increasing amounts of malonate resulted in a concentration-dependent decrease in the asymmetric labeling of alanine. When(3-13C)propionate oxidation was performed in the CS1- yeast cells containing CS1, CS1/MDH1, and CS1/HSA, the CS/HSA **transformant** displayed significantly decreased asymmetry in the labeling of the C2 and C3 positions of alanine (C3/C2 = 2.9). No significant difference was found between parental cells and the CS1 and CS1/MDH1 **transformants**. Growth experiments on rich medium did not show any differences between the **transformants**. On minimal medium, however, the CS1/HSA **transformant** displayed an increased doubling time. These data show that, in yeast cells containing the CS1/MDH1 fusion protein, symmetrical intermediates are transferred directly from TCA cycle enzyme to TCA cycle enzyme under in vivo conditions just as is observed in the parental cell. The data also show that it is possible to alter this effect in the TCA cycle pathway by introduction of a genetically engineered CS1/HSA fusion protein. We also discuss these data in the context of the metabolon hypothesis for the Krebs TCA cycle.

09454343 BIOSIS NO.: 199497462713
Overexpression and purification of the soluble polyhydroxyalkanoate **synthase** from Alcaligenes eutrophus: Evidence for a required posttranslational modification for catalytic activity.
AUTHOR: Gerngross T U; Snell K D; Peoples O P; Sinskey A J; Csuhai E; Masamune S; Stubbe J(a)
AUTHOR ADDRESS: (a)Dep. Chemistry, Massachusetts Inst. Technol., 77 Massachusetts Ave., Cambridge, MA 02139-4307**USA
JOURNAL: Biochemistry 33 (31):p9311-9320 1994
ISSN: 0006-2960
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Polyhydroxyalkanoate (PHA) **synthase** has been expressed in Escherichia coli by reengineering the 5'-end of the wild-type (wt) gene and subsequent **transformation** of this gene into protease-deficient E. coli UT5600(ompT-). Induction with IPTG results in soluble PHA **synthase**, which is apprx 5% of the total protein. The soluble **synthase** has been purified to gt 90% homogeneity using FPLC chromatography on hydroxylapatite and Q-Sepharose and has a specific activity of 5 mu-mol min-1 mg-1. The molecular weight of the PHA product is apprx 10-6 Da based on PlGel chromatography and calibration using polystyrene molecular weight markers. The **synthase** in the absence of substrate appears to exist in both monomeric and dimeric forms. Incubation of the **synthase** with an excess of substrate converts it into a form that is now extractable into CHCl-3 and sediments on sucrose density ultracetrifugation with PHA. Studies in which the ratio of substrate, 3-D-hydroxybutyrylCoA, to **synthase** is varied suggest that during polymerization the elongation process occurs at a rate much faster than during the initiation process. A mechanistic model has been proposed for the polymerization process (Griebel, R., Smith, Z., & Merrick, J. (1968) Biochemistry 7, 3676-3681)in which two cysteines are required for catalysis. This model is based on the well-characterized enzymes involved in fatty acid biosynthesis. To test this model, several site-directed mutants of **synthase**, selected based on sequence conservation among **synthases**, have been prepared. The C459S mutant has activity apprx 90% that of the wt protein, while the C319S and C319A **synthases** possess lt 0.01% the activity of the wt protein. CD and antibody studies suggest that the mutant proteins are properly folded. The detection of only a single essential cysteine by mutagenesis and the requirement for posttranslational modification by phosphopantetheine to provide a second thiol in many enzymes utilizing coenzyme A thiol ester substrates made us consider the possibility that posttranslational modification was required for **synthase** activity as well. This hypothesis was confirmed when the plasmid containing PHA **synthase** (pKAS4) was **transformed** in to E. coli SJ16, requiring beta-alanine for growth. Growth of SJ16/pKAS4 on (3H)-beta-alanine followed by Coomassie staining of the protein and autoradiography revealed that PHA **synthase** is overexpressed and that beta-alanine is incorporated into the protein. These results suggest PHA **synthase** is posttranslationally modified by phosphopantetheine. Mutagenesis studies and detection of phosphopantetheine suggest that the mechanistic model of Griebel et al. (1968) in which two thiols are required for catalysis is a reasonable starting point for the examination of the mechanism of the polymerization process.

2/7/15 (Item 15 from file: 5)
DIALOG(R)File 5:BIOSIS PREVIEWS(R)

07567401 BIOSIS NO.: 000091107955
RELATIONSHIP BETWEEN BODY SIZE GROWTH RATE AND MAXIMAL ENZYME ACTIVITIES IN THE BRINE SHRIMP ARTEMIA-FRANCISCANA

AUTHOR: BERGES J A; ROFF J C; BALLANTYNE J S
AUTHOR ADDRESS: DEP. ZOOL., UNIV. GUELPH, ONT. N1G 2W1, CAN.
JOURNAL: BIOL BULL (WOODS HOLE) 179 (3). 1990. 287-296.
FULL JOURNAL NAME: Biological Bulletin (Woods Hole)
CODEN: BIBUB
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Activity-body size relationships for eight enzymes (**citrate synthase**, CS: lactate dehydrogenase, LDH; pyruvate kinase, PK; alanine aminotransferase, ala AT; aspartate aminotransferase, asp AT; glutamate dehydrogenase. GDH; glucose-6-phosphate dehydrogenase, G6Pdh; and nucleoside diphosphate kinase, NDPK) were examined in the brine shrimp, Artemia franciscana. The animals were fed on the alga Dunaliella salina, which was provided in three concentrations representing a 25-fold range. Enzyme activities per animal (Y) were regressed against body size (M, expressed as dry mass or protein) in the form of the allometric equation, log Y = log a+b log M, where a and b are fitted constants. For all enzymes considered, the value of the scaling exponent (b) was significantly higher when dry mass was used, as a body size index, than when protein mass was used. Therefore, the index of body size chosen can influence the exponent obtained in allometric studies. Although specific growth rates of different cultures varied greatly, no significant differences in scaling relationships were found between cultures for any enzyme. For many enzymes, growth rate may not be a source of variation in scaling relationships. Unlike the other enzymes examined, the log-**transformed** NDPK activity versus log-**transformed** mass was not linear; NDPK activity reached a plateau. Variation in NDPK scaling relationships with growth may provide a means to predict growth rate in Artemia.

2/7/16 (Item 16 from file: 5)
DIALOG(R)File 5:BIOSIS PREVIEWS(R)

06752384 BIOSIS NO.: 000088061815
METABOLIC STUDIES ON **CITRATE SYNTHASE** MUTANTS OF YEAST A CHANGE IN PHENOTYPE FOLLOWING **TRANSFORMATION** WITH AN INACTIVE ENZYME
AUTHOR: KISPAL G; EVANS C T; MALLOY C; SRERE P A
AUTHOR ADDRESS: VA MED. CENT. RES. SERV. 151B , 4500 S. LANCASTER RD., DALLAS, TEXAS 75216.
JOURNAL: J BIOL CHEM 264 (19). 1989. 11204-11210.
FULL JOURNAL NAME: Journal of Biological Chemistry
CODEN: JBCHA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: We have studied the growth on acetate, the metabolism of acetate enzymes, and respiration of a series of **citrate synthase** mutants of Saccharomyces cerevisiae. The results confirmed and extended our previous observation that cytosolic **citrate synthase** is not neccessary for growth on acetate. Deletion of mitochondrial **citrate synthase** (CS1) protein resulted in changes in metabolites, decrease in the amounts of pyruvate and .alpha.-ketoglutarate dehydrogenase complexes, reduced mitochondrial respiration of **citrate** and isocitrate, and an inability to grow on acetate. Using site-directed mutagenesis, we constructed two separate CS1 proteins with mutations in the enzyme's active site. The mitochondria of cells carrying either site-directed mutagenized CS1 contained the inactive **citrate synthase** protein. With one mutant in which His313 was replaced with a glycine (CS1/H313G), growth on acetate was restored, and mitochondrial respiration of **citrate** and isocitrate increased toward parental levels as did the levels of several enzymes. With the other mutant CS1 in which Asp414 was replaced with a glycine (CS1/D414G), no growth on acetate or changes in other parameters was

observed. We propose that the characteristics of the strain carrying the CS1 with a H313G mutation result from the formation of an intact Krebs cycle complex by the inactive but structurally unchanged H313G protein.

2/7/17 (Item 17 from file: 5)
DIALOG(R)File 5:BIOSIS PREVIEWS(R)

06749825 BIOSIS NO.: 000088059256
THE MECHANISM OF PYRUVATE SYNTHESIS FROM GLYCEROL BY YARROWIA-LIPOLYTICA
AUTHOR: MORGUNOV I G; ERMAKOVA I T
AUTHOR ADDRESS: INST. BIOCHEM. PHYSIOL. MICROORG., ACAD. SCI. USSR, PUSHCHINO, USSR.
JOURNAL: MIKROBIOLOGIYA 58 (1). 1989. 26-30.
FULL JOURNAL NAME: Mikrobiologiya
CODEN: MIKBA
RECORD TYPE: Abstract
LANGUAGE: RUSSIAN

ABSTRACT: The work was concerned with assaying the activity of enzymes involved in the central and anapleurotic pathways functioning in Yarrowia lipolytica cells in the biosynthesis of .alpha.-keto acids when the growth was retarded due to thiamine deficiency. The activities of enzymes catalysing the primary reactions of glycerol assimilation as well as further glycerol **transformation** to pyruvate in the reactions of glycolysis were shown to remain at the same level as in the exponential growth phase. Thiamine deficiency causes a drop in the activities of pyruvate and .alpha.-ketoglutarate dehydrogenases which contain thiamine pyrophosphate as a cofactor. The reaction of pyruvate conversion into acetyl CoA becomes a limiting step in the metabolism and, as a result, most of the acid being formed is released from the cell into the cultural broth. The break in the tricarboxylic acid cycle at the level of .alpha.-ketoglutarate dehydrogenase leads to .alpha.-ketoglutarate excretion. The high ratio between pyruvic and .alpha.-ketoglutaric acid is due to the decreased intensity of the tricarboxylic acid cycle operation and, consequently, of .alpha.-ketoglutarate synthesis owing to the low activity as pyruvate dehydrogenase as pyruvate carboxylase and pyruvate decarboxylase, enzymes involved in the anapleurotic pathways for the synthesis of oxalacetic acid and acetyl CoA which are substrates for **citrate synthase**, the key enzyme of the cycle.

2/7/18 (Item 18 from file: 5)
DIALOG(R)File 5:BIOSIS PREVIEWS(R)

05201494 BIOSIS NO.: 000082042116
IMMUNOCYTOCHEMICAL ANALYSIS SHOWS THAT GLYOXYSOMES ARE DIRECTLY **TRANSFORMED** TO LEAF PEROXISOMES DURING GREENING OF PUMPKIN COTYLEDONS
AUTHOR: NISHIMURA M; YAMAGUCHI J; MORI H; AKAZAWA T; YOKOTA S
AUTHOR ADDRESS: RES. INST. BIOCHEM. REGULATION, SCH. AGRICULTURE, NAGOYA UNIV., CHIKUSA, NAGOYA 464, JPN.
JOURNAL: PLANT PHYSIOL (BETHESDA) 81 (1). 1986. 313-316.
FULL JOURNAL NAME: Plant Physiology (Bethesda)
CODEN: PLPHA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The functional transition of glyoxysomes to leaf peroxisomes occurs during greening of germinating pumpkin cotyledons (Cucurbita sp. Amakuri Nankin). The immunocytochemical protein A-gold method was employed in the analysis of the transition using glyoxysomal specific **citrate synthase** immunoglobulin G and leaf peroxisomal specific glycolate oxidase immunoglobulin G. The labeling density of

citrate synthase was decreased in the microbodies during the greening, whereas that of glycolate oxidase was dramatically increased. Double labeling experiments using different sizes of protein A-gold particles show that both the glyoxysomal and the leaf peroxisomal enzymes coexist in the microbody of the transitional stage indicating that glyoxysomes are directly **transformed** to leaf peroxisomes during greening.

2/7/19 (Item 19 from file: 5)
DIALOG(R)File 5:BIOSIS PREVIEWS(R)

04276920 BIOSIS NO.: 000078006462
CHARACTERIZATION OF GLYOXYSOMES IN YEASTS AND THEIR **TRANSFORMATION** INTO PEROXISOMES IN RESPONSE TO CHANGES IN ENVIRONMENTAL CONDITIONS
AUTHOR: ZWART K B; VEENHUIS M; PLAT G; HARDER W
AUTHOR ADDRESS: DEP. MICROBIOL., BIOL. CENTRE, UNIV. GRONINGEN, KERKLAAN 30, NL-9751 NN HAREN, NETHERLANDS.
JOURNAL: ARCH MICROBIOL 136 (1). 1983. 28-38.
FULL JOURNAL NAME: Archives of Microbiology
CODEN: AMICC
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: During growth of the yeasts Candida utilis and Hansenula polymorpha in mineral media containing ethanol as a C source and ammonium sulfate as a N source, the specific activities of isocitrate lyase and malate **synthase** were significantly increased when compared to glucose/ammonium sulfate-grown cells. In addition to the enhanced levels of these glyoxylate cycle enzymes, an increase in the specific activities of D-amino acid oxidase, amine oxidase or urate oxidase was observed when ammonium sulfate in the ethanol medium was replaced by D-alanine, methyl- or ethylamine or uric acid. The subcellular localization of these enzymes was investigated by cell fractionation studies involving homogenization of protoplasts followed by differential and sucrose gradient centrifugation. In ethanol/ammonium sulfate-grown cells, isocitrate lyase and malate **synthase** cosedimented in a fraction together with catalase and part of the malate dehydrogenase. EM revealed that this fraction consisted of microbodies which must be regarded as glyoxysomes. Two other glyoxylate cycle enzymes, **citrate synthase** and aconitase together with the other part of malate dehydrogenase, cosedimented with cytochrome c oxidase, a mitochondrial marker enzyme. In ethanol/D-alanine-, ethanol/methylamine- or ethanol/ethylamine-grown C. utilis and ethanol/uric acid-grown H. polymorpha, a peroxisomal enzyme, i.e., D-amino acid oxidase, amine oxidase or uric acid oxidase cosedimented with the glyoxysomal key enzymes. Cytochemical staining experiments demonstrated that in these variously-grown cells the activities of the oxidases were confined to the microbody-matrix; this also contained malate **synthase** activity. Transfer of C. utilis cells from glucose/ammonium sulfate- into ethanol/ammonium sulfate-containing media resulted in an increase in the original size and volume fraction of the microbodies. A further increase was observed when ammonium sulfate was replaced by methylamine. Essentially similar results were obtained with H. polymorpha cells. In neither of the 2 organisms, indications of de novo synthesis of microbodies was obtained during transfer experiments. Invariably the microbodies developing in cells placed in the new environment originated from organelles already present in the inoculum cells by import of the substrate-specific enzyme protein(s). The combined results of biochemical, cytochemical and EM experiments showed that in the yeasts studied under appropriate conditions glyoxysomal and peroxisomal enzyme activities were localized in one and the same microbody, rather than in separate organelles.

2/7/20 (Item 20 from file: 5)

DIALOG(R)File 5:BIOSIS PREVIEWS(R)
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02726843 BIOSIS NO.: 000068037441
EFFECT OF LIGHT ON THE DEVELOPMENT OF GLYOXYSOMAL FUNCTIONS IN THE MUSTARD SINAPIS-ALBA SEEDLINGS
AUTHOR: BAJRACHARYA D; SCHOPFER P
AUTHOR ADDRESS: BIOL. INST. II UNIV. FREIB., SCHAENZLESTR. 1, D-7800 FREIBURG, W. GER.
JOURNAL: PLANTA (BERL) 145 (2). 1979. 181-186.
FULL JOURNAL NAME: PLANTA (Berlin)
CODEN: PLANA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The degradation of storage fat in the cotyledons of mustard seedlings is unaffected by phytochrome and photosynthesis (irradiation with continuous red or far-red light from sowing of the seeds) although light imposes a strong constraint on the translocation of organic matter from the cotyledons into the seedling axis. Likewise, the development and disappearance of glyoxysomal enzyme activities (isocitrate lyase, malate **synthase**, **citrate synthase**) takes place independently of light. The mobilization of storage fat (fat .fwdarw. carbohydrate **transformation**) is independent of photomorphogenesis. The surplus of carbohydrate produced from fat in the light seems to be converted to starch grains in the plastids, which function as a secondary storage pool in the cotyledons.

2/7/21 (Item 21 from file: 5)
DIALOG(R)File 5:BIOSIS PREVIEWS(R)
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02421144 BIOSIS NO.: 000066003685
METABOLIC REGULATION OF INITIAL REACTIONS OF THE TRI CARBOXYLIC CYCLE
AUTHOR: GULYI M F
AUTHOR ADDRESS: A.V. PALLADIN INST. BIOCHEM., ACAD. SCI. UKR. SSR, KIEV, USSR.
JOURNAL: UKR BIOKHIM ZH 49 (5). 1977 (RECD 1978) 115-129.
FULL JOURNAL NAME: Ukrayins'kyi Biokhimichnyi Zhurnal
CODEN: UBZHA
RECORD TYPE: Abstract
LANGUAGE: RUSSIAN

ABSTRACT: Changes in intensity and direction of the reactions in the tricarboxylic cycle in bacteria, fungi and mammals under the effect of different regulatory effects are accompanied by changes in the reactions not only in the tricarboxylic cycle itself but also in many other metabolic processes and may be in the whole intracellular metabolism. For the **citrate** cycle the regulation of 2 initial reactions of the cycle, **citrate synthetase** and isocitrate dehydrogenase, is of the greatest importance. The **citrate synthetase** reaction is inhibited by the long-chain CoA acyl derivatives, namely: stearyl-, palmityl-, oleoyl-CoA and others lowering affinity of the enzyme for oxaloacetic acid as well as by ATP and other nucleoside phosphates lowering affinity of the enzyme for acetyl-CoA and NADH. An inhibitory effect of ATP and **citrate synthetase** was disputed by others, considering that accumulating NADH rather than ATP produces an inhibitory effect. Acetyl-CoA and oxaloacetic acid are activators of **citrate synthetase**; .alpha.-ketoglutaric acid being an allosteric inhibitor suppresses the enzyme. Glyoxylic acid reacting with oxaloacetic acid produces oxalomalic acid and inhibits **citrate transformation**, blocking aconitase. There exist NAD- and NADP-dependent isocitrate dehydrogenases. The former is localized in mitochondria, the latter in cytosol and mitochondria. Cytosol and mitochondria NADP-isoenzymes differ electrophoretically and immunochemically. NADP-dependent isocitrate

dehydrogenase dehydrates reversibly isocitrate to oxalsuccinic acid and splits the latter into .alpha.-ketoglutarate and CO2. The enzyme consists of 2 subunits and is activated by Mn2+, AMP and ADP, inhibited by ATP and other nucleoside triphosphates as well as by a mixture of glyoxylic and oxaloacetic acids. A direct reaction is regulated by the CO2 level in the tissues. NADP-dependent isocitrate dehydrogenase is considered to be important for providing the acetyl-CoA and NADP transport through the mitochondrial membranes as well as for synthesis of tricarboxylic acids at the expense of .alpha.-ketoglutarate and as a generator of NADPH for the reductive processes. The NAD-dependent enzyme catalyzes the same process as the NADP-enzyme but irreversibly and is active in microorganisms only in the presence of AMP. The NAD-dependent enzyme of the animal tissues does not demand an obligatory presence of AMP but is activated by this nucleotide as well as by Mg2+, **citrate**, isocitrate and is inhibited by .alpha.-ketoglutarate.

2/7/22 (Item 1 from file: 73)
DIALOG(R)File 73:EMBASE

06897259 EMBASE No: 1997181640
Aluminum tolerance in **transgenic plants** by alteration of **citrate** synthesis
De la Fuente J.M.; Ramirez-Rodriguez V.; Cabrera-Ponce J.L.; Herrera-Estrella L.
L. Herrera-Estrella, Departamento de Ingenieria Genetica, CIEA (CINVESTAV), Unidad Irapuato, Apdo. Postal 629, (36500) Irapuato, Glo Mexico
Science (SCIENCE) (United States) 1997, 276/5318 (1566-1568)
CODEN: SCIEA ISSN: 0036-8075
DOCUMENT TYPE: Journal; Article
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH
NUMBER OF REFERENCES: 20

Aluminum when in soluble form, as found in acidic soils that comprise about 40 percent of the world's arable land, is toxic to many crops. Organic acid excretion has been correlated with aluminum tolerance in higher **plants**. Overproduction of **citrate** was shown to result in aluminum tolerance in **transgenic** tobacco (Nicotiana tabacum) and papaya (Carica papaya) **plants**.

2/7/23 (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

10068358 99356779
Over expression of mitochondrial **citrate synthase** gene improves the growth of carrot cells in Al-phosphate medium.
Koyama H; Takita E; Kawamura A; Hara T; Shibata D
Laboratory of Plant Cell Technology, Faculty of Agriculture, Gifu University, Japan. koyama@cc.gifu-u.ac.jp
Plant Cell Physiol (JAPAN) May 1999, 40 (5) p482-8, ISSN 0032-0781
Journal Code: B1G
Languages: ENGLISH
Document type: JOURNAL ARTICLE
A mitochondrial **citrate synthase** (CS) of Arabidopsis thaliana was introduced into carrot (Daucus carota L. cv. MS Yonsun) cells by Agrobacterium tumefaciens-mediated **transformation**. **Transgenic** cell lines had high CS activity, the highest value observed was 0.24 mumol (mg protein)-1 min-1 which was 1.9-fold of that in wild-type cells. Transcript levels of DcCS were similar between **transgenic** lines, but those of AtCS were increased as the CS activity of cells was increased. Isoelectric focussing revealed that the CS polypeptide of the **transgenic** lines had a pI value different from that of the wild-type

cells, although the molecular mass was the same. These results indicate that the CS polypeptides of A. thaliana were expressed and processed to the mature form in carrot cells. The growth rate and excretion was 2.2-2.8 and 2.8-4.0 fold greater in the **transgenic** cells than in the wild type cells, respectively. Phosphate uptake from Al-phosphate also increased in **transgenic** cells. It appears, the overexpression of mitochondrial **citrate synthase** in carrot cells improves the growth rate in Al-phosphate medium possibly as a result of increased **citrate** excretion.

2/7/24 (Item 2 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
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09824164 99074814
Effect of dietary fat on lymphocyte proliferation and metabolism.
Otton R; Graziola F; Souza JA; Curi TC; Hirata MH; Curi R
Department of Physiology and Biophysics, University of Sao Paulo, Butantan, Brazil.
Cell Biochem Funct (ENGLAND) Dec 1998, 16 (4) p253-9, ISSN 0263-6484 Journal Code: C9W
Languages: ENGLISH
Document type: JOURNAL ARTICLE
The effect of diets enriched with fat containing different fatty acids on glucose and glutamine metabolism of mesenteric lymph nodes lymphocytes, spleen, and thymus and lymphocyte proliferation was examined. The following fat-rich diets were tested: (1) standard chow (CC); (2) medium chain saturated fatty acids (MS)--coconut fat oil; (3) long chain saturated fatty acids (LS)--cocoa butter; (4) monounsaturated fatty acids (MU)--canola oil (n-9); (5) polyunsaturated fatty acids (PU)--soybean oil (n-6). Of the fat-rich diets tested, MS was the one to present the least pronounced effect. Lymphocyte proliferation was reduced by LS (64 per cent), MU (55 per cent), and PU (60 per cent). Hexokinase activity was enhanced in lymph node lymphocytes by PU (67 per cent), in the spleen by MS (42 per cent), and in the thymus by PU (30 per cent). This enzyme activity was reduced in the spleen (33 per cent) by LS and MU (35 per cent). In the thymus, this enzyme activity was reduced by LS (26 per cent) and MU (13 per cent). Maximal phosphate-dependent glutaminase activity was raised in lymphocytes by MS (70 per cent) and MU (20 per cent). This enzyme activity, however, was decreased in lymphocytes by PU (26 per cent), in the spleen by LS (15 per cent), and in the thymus by MU (44 per cent). **Citrate synthase** activity was increased in lymphocytes by MU (35 per cent), in the spleen by LS (56 per cent) and MU (68 per cent), and in the thymus by LS (42 per cent). This enzyme activity was decreased in lymphocytes by PU (24 per cent) only. [U-14C]-Glucose decarboxylation was raised by all fat-rich diets; MS (88 per cent). LS (39 per cent), MU (33 per cent), and PU (50 per cent), whereas [U-14C]-glutamine decarboxylation was increased by LS (53 per cent) and MU (55 per cent) and decreased by MS (17 per cent). The results presented indicate that the reduction in lymphocyte proliferation due to LS, LU and PU could well be a consequence of changes in glucose and glutamine metabolism.

2/7/25 (Item 1 from file: 10)
DIALOG(R)File 10:AGRICOLA
(c) format only 1999 The Dialog Corporation. All rts. reserv.

3616777 20598209 Holding Library: AGL
Nitrate acts as a signal to induce organic acid metabolism and repress starch metabolism in tobacco
Scheible, W.R. Gonzalez-Fontes, A.; Lauerer, M.; Muller-Rober, B.; Caboche, M.; Stitt, M.
Universitat Heidelberg, Heidelberg, Germany.
[Rockville, MD : American Society of Plant Physiologists, c1989-
The Plant cell. May 1997. v. 9 (5) p. 783-798.

ISSN: 1040-4651 CODEN: PLCEEW
DNAL CALL NO: QK725.P532
Language: English
Includes references
Place of Publication: Maryland
Subfile: IND; OTHER US (NOT EXP STN, EXT, USDA; SINCE 12/76);
Document Type: Article

Nia30(145) **transformants** with very low nitrate reductase activity provide an in vivo screen to identify processes that are regulated by nitrate. Nia30(145) resembles nitrate-limited wild-type **plants** with respect to growth rate and protein and amino acid content but accumulates large amounts of nitrate when it is grown on high nitrate. The transcripts for nitrate reductase (NR), nitrite reductase, cytosolic glutamine **synthetase**, and glutamate **synthase** increased; NR and nitrite reductase activity increased in leaves and roots; and glutamine **synthetase** activity increased in roots. The transcripts for phosphoenolpyruvate carboxylase, cytosolic pyruvate kinase, **citrate synthase**, and NADP-isocitrate dehydrogenase increased; phosphoenolpyruvate carboxylase activity increased; and malate, **citrate**, isocitrate, and alpha-oxoglutarate accumulated in leaves and roots. There was a decrease of the ADP-glucose pyrophosphorylase transcript and activity, and starch decreased in the leaves and roots. After adding 12 mM nitrate to nitrate-limited Nia30(145), the transcripts for NR and phosphoenolpyruvate carboxylase increased, and the transcripts for ADP-glucose pyrophosphorylase decreased within 2 and 4 hr, respectively. Starch was remobilized at almost the same rate as in wildtype **plants**, even though growth was not stimulated in Nia30(145). It is proposed that nitrate acts as a signal to initiate coordinated changes in carbon and nitrogen metabolism.

2/7/26 (Item 1 from file: 203)
DIALOG(R)File 203:AGRIS

01757808 AGRIS No: 94-034748
Effect of lead arsenate on **citrate synthase** activity in fruit pulp of satsuma mandarin
Yamaki, Y.T. (Tokyo Univ. (Japan). Faculty of Agriculture)
Journal: Journal of the Japanese Society for Horticultural Science, Mar 1990, v. 58(4) p. 899-905
Notes: 3 tables; 3 fig.; 28 ref. ISSN: 0013-7626
Language: Japanese Summary Language: English, Japanese
Place of Publication: Japan
Document Type: Journal Article, Summary
Journal Announcement: 2004 Record input by Japan

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PLEASE ENTER A COMMAND OR BE LOGGED OFF IN 5 MINUTES
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Set	Items	Description
S1	40	(TRANSGENIC? OR TRANSFORM?) AND (PLANT OR PLANTS) AND CITRATE AND (SYNTHASE? OR SYNTHETASE?)
S2	26	RD (unique items)

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Set	Items	Description
S1	40	(TRANSGENIC? OR TRANSFORM?) AND (PLANT OR PLANTS) AND CITRATE AND (SYNTHASE? OR SYNTHETASE?)
S2	26	RD (unique items)

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Set Items Description

S1 40 (TRANSGENIC? OR TRANSFORM?) AND (PLANT OR PLANTS) AND CITRATE AND (SYNTHASE? OR SYNTHETASE?)

S2 26 RD (unique items)

13/7/47 (Item 2 from file: 35)
DIALOG(R)File 35:Dissertation Abstracts Online

1035603 ORDER NO: AAD88-27397
A BIOCHEMICAL AND GENETIC INVESTIGATION OF THE EXPRESSION OF MITOCHONDRIAL **CITRATE SYNTHASE** IN SELECTED **PLANT** SYSTEMS
Author: UNGER, ERICA ANN
Degree: PH.D.
Year: 1988
Corporate Source/Institution: RUTGERS UNIVERSITY THE STATE U. OF NEW JERSEY (NEW BRUNSWICK) (0190)
DIRECTOR: AUREA C. VASCONCELOS
Source: VOLUME 49/10-B OF DISSERTATION ABSTRACTS INTERNATIONAL. PAGE 4105. 137 PAGES

Citrate synthase catalyzes the condensation of acetyl-coenzyme A and oxaloacetate in the initial step of the tricarboxylic acid cycle, which occurs in the mitochondrial matrix. In these investigations, this enzyme was used to represent the activity of this cycle during physiologically variant conditions. Biochemical experimentation resulted in the purification of **citrate synthase** and the production of competent antiserum. Immunoblot analysis indicated that of **citrate synthase** was present in all of tissues examined. Additionally, an increase in **citrate synthase** enzyme activity was observed in response to light. The genetic aspect of **citrate synthase** expression involved the isolation of a complementary **DNA** clone **encoding** this polypeptide. Through nucleic acid hybridization studies, it was determined that there are at least two **genes** that **encode** this protein in the small crucifer, Arabidopsis thaliana. Additionally, genomic clones **encoding** these two **genes** have been isolated. Transcription of **citrate synthase** was examined to further investigate the effects of light on this enzyme. Analysis of the data provided from these investigations allows for a hypothesis concerning the expression and regulation of **citrate synthase** to be presented. From these data it was inferred that the initial steps in the tricarboxylic acid cycle were active in the light and that the mode of regulation concerning the positive response **citrate synthase** activity exhibited following illumination, may involve either new synthesis or the activation of existing molecules.

13/7/48 (Item 3 from file: 35)
DIALOG(R)File 35:Dissertation Abstracts Online

794172 ORDER NO: AAD82-24924
PHYSIOLOGICAL AND METABOLIC STUDIES ON PHOTOINDUCED GERMINATION OF ONOCLEA SENSIBILIS SPORES
Author: CHEN, CHIN-YU
Degree: PH.D.
Year: 1982
Corporate Source/Institution: THE UNIVERSITY OF MICHIGAN (0127)
Source: VOLUME 43/06-B OF DISSERTATION ABSTRACTS INTERNATIONAL. PAGE 1683. 225 PAGES

The present work is aimed at analyzing the physiological and metabolic nature of the germination processes before and after photoinduction.

01423806 ORDER NO: AADAA-I9522255

PHYSIOLOGICAL AND MOLECULAR GENETIC STUDIES OF CITRIC ACID ACCUMULATION IN CITRUS FRUITS (CITRUS MAXIMA, CITRUS RETICULATA)

Author: CANEL, CAMILO
Degree: PH.D.
Year: 1994
Corporate Source/Institution: UNIVERSITY OF CALIFORNIA, RIVERSIDE (0032)
Chairperson: MIKEAL L. ROOSE
Source: VOLUME 56/03-B OF DISSERTATION ABSTRACTS INTERNATIONAL.
PAGE 1217. 180 PAGES

Acitric is the **gene** responsible for the acidless phenotype of pummelo 2240 (Citrus maxima (Burm.) Merrill). In order to identify acitric, aspects of citrate biosynthesis and transport were studied in high- and low-acid individuals of populations in which acitric segregates, and their progenitors, pummelo 2240, Kinnow mandarin (C. reticulata Blanco, hybrid King x Willowleaf), and Chandler pummelo (C. maxima (Burm.) Merrill, hybrid Siamese sweet 2240 x Kao Pan 2241).

Tonoplast vesicles isolated from juice cells of low-acid individuals by differential centrifugation, incorporated more ($\sp{14}$C) citrate than did vesicles from high-acid fruits. Uptake of ($\sp{14}$C) citrate occurred against a concentration gradient, was stimulated by nitrate-sensitive ATP hydrolysis, was not inhibited by malate and only slightly by isocitrate. Uptake was not stimulated by hydrolysis of PPi, and was not affected by the ionophore nigericin, indicating that citrate transport is not driven by a trans-tonoplast electrochemical gradient. No evidence was found of a defective citrate transport mechanism at the tonoplast of juice cells of acidless fruits.

Two proteins were identified in membrane fractions of low-acid juice that were not detected in high-acid fractions. The **encoding** cDNAs were isolated from a juice-tissue expression library by immunoscreening. The **genes**, designated asr1 and hsp20, are homologous to **plant genes encoding** ripening-induced and heat-shock proteins, respectively. Preferential expression of asr1 and hsp20 in developing low-acid fruits may reflect their inability to accumulate citric acid.

Juice-tissue cDNAs **encoding** the mitochondrial **citrate synthase** (CS) of pummelo 2240 were cloned by RT-PCR. Quantitative detection of cit poly(A)$\sp+$ mRNA showed that transcript levels are not developmentally regulated in juice tissues; no differences were observed between high- and low-acid genotypes. Hybridization studies revealed that citrus has only one copy of cit, and that cit transcription in juice tissues produces a single 1.85-kb mRNA.

Segregation of RFLPs associated with cit, asr1, and hsp20 did not correlate with fruit acidity, indicating that none of these **genes** is acitric. The mitochondrial localization of CS in juice cells is evidence that the accumulating citric acid originates in the mitochondria, and that the TCA cycle has the dual role of energy generator and supplier of citrate molecules for export to the vacuole. At the tonoplast, citric acid accumulation is then mediated by a carrier that uses energy released during ATP hydrolysis to actively and specifically import citrate.

Physiological studies point out that (a) a temporal **sequence** of events after photoinduction can be constructed from the data with inhibitors, (b) at about 12 hours after photoinduction, the germination processes appear to enter into an irreversible phase, (c) a broad pH optimum is found for spore germination, in the range of pH 4 to 10.5, but this is in part caused by the ability of spores to change the medium pH toward neutrality, and (d) light treatment induces rapid acidification of the medium (t(, 1/2) = 5-10 min) followed by slow alkalinization (t(, 1/2) = 1-2 hours) immediately after photoinduction.

Metabolic studies were directed towards analyses of sucrose catabolism and energy metabolism. These studies indicate that (a) hexokinase, P-fructokinase, pyruvate kinase, pyruvate dehydrogenase + **citrate synthase**, and a step that feeds (alpha)-ketoglutarate from glutamate are poised as non-equilibrium steps in all germination stage examined, and all other tested enzymes are equilibrium or near equilibrium types, (b) dry spores contain an additional, non-equilibrium reaction at the step catalyzed by glyceraldehyde-3-P dehydrogenase + P-glycerate kinase, which changes to an equilibrium type after dark soaking, (c) dark soaking acts to increase the activity of NADP-isocitrate dehydrogenase nearly 3 fold, but not other enzymes examined, (d) photoinduction causes less changes in metabolite profiles and no change in enzyme activities when compared with the effects of dark soaking, and (e) anaerobiosis drastically increases the contents of pyruvate and (alpha)-ketoglutarate, regardless of when it is given.

All results are discussed in the light of other data in the literature, and a possible mechanism of photoinduction is proposed.

13/7/9 (Item 9 from file: 5)
DIALOG(R)File 5:BIOSIS PREVIEWS(R)

09131029 BIOSIS NO.: 199497139399
Nodulating ability of Rhizobium tropici is conditioned by a plasmid-**encoded citrate synthase**.
AUTHOR: Pardo Marco A; Lagunez Jaime; Miranda Juan; Martinez Esperanza(a)
AUTHOR ADDRESS: (a)Dep. Genetica Mol., Centro de Investigacion sobre Fijacion de Nitrogeno, UNAM, Ap.P. 565-A, Cuer**Mexico
JOURNAL: Molecular Microbiology 11 (2):p315-321 1994
ISSN: 0950-382X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Rhizobium species elicit the formation of nitrogen-fixing root nodules through a complex interaction between bacteria and **plants**. Various bacterial **genes** involved in the nodulation and nitrogen-fixation processes have been described and most have been localized on the symbiotic plasmids (pSym). We have found a **gene encoding citrate synthase** on the pSym plasmid of Rhizobium tropici, a species that forms nitrogen-fixing nodules on the roots of beans (Phaseolus vulgaris) and trees (Leucaena spp.). **Citrate synthase** is a key metabolic enzyme that incorporates carbon into the tricarboxylic acid cycle by catalysing the condensation of acetyl-CoA and oxaloacetic acid to form citrate. R. tropici pcsA (the plasmid **citrate synthase gene**) is closely related to the corresponding **genes** of Proteobacteria. pcsA inactivation by a Tn5-mob insertion causes the bacteria to form fewer nodules (30-50% of the original strain) and to have a decreased **citrate synthase** activity in minimal medium with sucrose. A clone carrying the pcsA **gene** complemented all the phenotypic alterations of the pcsA mutant, and conferred Rhizobium leguminosarum bv. phaseoli (which naturally lacks a plasmid **citrate synthase gene**) a higher nodulation and growth capacity in correlation with a higher **citrate synthase** activity. We have also found that pcsA **gene** expression is sensitive to iron availability, suggesting a possible role of pcsA in iron uptake.

13/7/29 (Item 29 from file: 5)
DIALOG(R)File 5:BIOSIS PREVIEWS(R)

06883776 BIOSIS NO.: 000089037704
ISOLATION OF A COMPLEMENTARY **DNA ENCODING** MITOCHONDRIAL **CITRATE SYNTHASE** FROM ARABIDOPSIS-THALIANA
AUTHOR: UNGER E A; HAND J M; CASHMORE A R; VASCONCELOS A C
AUTHOR ADDRESS: MOLECULAR CELL BIOL., U125, UNIV. CONN., STORRS, CT 06268, USA.
JOURNAL: PLANT MOL BIOL 13 (4). 1989. 411-418.
FULL JOURNAL NAME: Plant Molecular Biology
CODEN: PMBID
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: We isolated a **cDNA** clone from Arabidopsis thaliana **encoding** the TCA cycle enzyme, **citrate synthase**. The **plant** enzyme displays 48% and 44% amino acid residue similarity with the pig, and yeast polypeptides, respectively. Many proteins, including **citrate synthase**, which are destined to reside in organelles such as mitochondria and chloroplasts, are the products of the nucleocytoplasmic protein synthesizing machinery and are imported post-translationally to the site of function. We present preliminary investigations toward the establishment of an in vitro **plant** mitochondrial import system allowing for future studies to dissect this process in **plants** where the cell must differentiate between mitochondria and chloroplast and direct their polypeptides appropriately.

? t s8/7/1-10

8/7/1 (Item 1 from file: 5)
DIALOG(R)File 5:BIOSIS PREVIEWS(R)

09738770 BIOSIS NO.: 199598193688
Correction of PREVIEWS 97551017. Metabolic studies on Saccharomyces cerevisiae containing fused **citrate synthase**/malate dehydrogenase. Addition of author name. Erratum published in BIOCHEMISTRY Vol. 33. Iss. 49. 1994. p. 14948.
AUTHOR: Lindbladh Christer; Brodeur Richard D; Small William C; Lilius G; Bulow Leif; Mosbach Klaus; Srere Paul A(a)
AUTHOR ADDRESS: (a)Pre-Clin. Sci. Unit, Dep. Veterans Aff. Med. Cent., 4500 S. Lancaster Rd., Dallas, TX 75216**USA
JOURNAL: Biochemistry 33 (39):p11684-11691 1994
ISSN: 0006-2960
DOCUMENT TYPE: Article; Erratum
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: We have constructed two different fusion proteins consisting of the C-terminal end of CS1 fused in-frame to the N-terminal end of MDH1 and HSA, respectively. The fusion proteins were expressed in mutants of Saccharomyces cerevisiae in which CS1 and MDH1 had been deleted and the phenotypes of the transformants characterized. The results show that the fusion proteins are transported into the mitochondria and that they restore the ability for the yeast mutants CS1-, MDH1-, and CS1-/MDH1- to grow on acetate. Determination of CS1 activity in isolated mitochondria showed a 10-fold increase for the strain that expressed native CS1, relative to the parental. In the transformant with CS1/MDH1 fusion protein, parental levels of CS1 were observed, while one-fifth this amount was observed for the strain expressing the CS1/HSA conjugate. Oxygen consumption studies on isolated mitochondria did not show any significant differences between parental-type yeast and the strains expressing the different fusion proteins or native CS1. (3-13C)Propionate was used to study the Krebs TCA cycle metabolism of yeast cells containing CS1/MDH1 fusion constructs. The 13C NMR study was performed in respiratory-competent parental yeast cells and using the **genetically** engineered yeast cells consisting of CS1- mutants expressing native CS1 and the fusion proteins CS1/MDH1 and CS1/HSA, respectively. (3-13C)Propionate is believed to be metabolized to (2-13C)succinyl-CoA before it enters the TCA cycle in the mitochondria. This metabolite is then oxidized through two symmetrical intermediates, succinate and fumarate, followed by conversion to malate, oxalacetate, and other metabolites such as alanine. If the symmetrical intermediates randomly diffuse between the enzymes in the mitochondria, the 13C label should be equally distributed on the C2 and C3 positions of malate and alanine. However, if succinate and fumarate are directly transferred with conserved orientation between the active sites of the enzymes succinate thiokinase, succinate dehydrogenase, and fumarase, the labeling of the C2 and C3 positions of malate, oxalacetate, and alanine will be asymmetrical. During oxidation of (3-13C)propionate in parental cells, we observed an asymmetric labeling of the C2 and C3 positions of alanine where the 13C enrichment was significantly higher in the C3 position (C3/C2 = 14.3). Inhibition of succinate dehydrogenase with increasing amounts of malonate resulted in a concentration-dependent decrease in the asymmetric labeling of alanine. When (3-13C)propionate oxidation was

performed in the CS1- yeast cells containing CS1, CS1/MDH1, and CS1/HSA, the CS/HSA transformant displayed significantly decreased asymmetry in the labeling of the C2 and C3 positions of alanine (C3/C2 = 2.9). No significant difference was found between parental cells and the CS1 and CS1/MDH1 transformants. Growth experiments on rich medium did not show any differences between the transformants. On minimal medium, however, the CS1/HSA transformant displayed an increased doubling time. These data show that, in yeast cells containing the CS1/MDH1 fusion protein, symmetrical intermediates are transferred directly from TCA cycle enzyme to TCA cycle enzyme under in vivo conditions just as is observed in the parental cell. The data also show that it is possible to alter this effect in the TCA cycle pathway by introduction of a **genetically** engineered CS1/HSA fusion protein. We also discuss these data in the context of the metabolon hypothesis for the Krebs TCA cycle.

8/7/2 (Item 2 from file: 5)
DIALOG(R)File 5:BIOSIS PREVIEWS(R)

09580254 BIOSIS NO.: 199598035172
Twelve Open Reading Frames Revealed in the 23.6 kb Segment Flanking the Centromere on the Saccharomyces cerevisiae Chromosome XIV Right Arm.
AUTHOR: Verhasselt Peter(a); Aert Rita; Voet Marleen; Volckaert Guido
AUTHOR ADDRESS: (a)Univ. Leuven, Lab. Gene Technol., Willem Croylaan 42, B-3001 Leuven**Belgium
JOURNAL: Yeast 10 (10):p1355-1361 1994
ISSN: 0749-503X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The nucleotide **sequence** of 23.6 kb of the right arm of chromosome XIV is described, starting from the centromeric region. Both strands were **sequenced** with an average redundancy of 4-87 per base pair. The overall G+C content is 38.8% (42.5% for putative coding regions versus 29-4% for non-coding regions). Twelve open reading frames (ORFs) greater than 100 amino acids were detected. Codon frequencies of the twelve ORFs agree with codon usage in Saccharomyces cerevisiae and all show the characteristics of low level expressed **genes**. Five ORFs (N2019, N2029, N2031, N2048 and N2050) are **encoded** by previously **sequenced genes** (the mitochondrial **citrate synthase gene**, FUN34, RPC34, PRP2 and URK1, respectively). ORF N2052 shows the characteristics of a transmembrane protein. Other elements in this region are a tRNA-Pro **gene**, a tRNA-Asn **gene**, a tau-34 and a truncated delta-34 element. Nucleotide **sequence** comparison results in relocation of the SIS1 **gene** to the left arm of the chromosome as confirmed by colinearity analysis. The nucleotide **sequence** data reported in this paper will appear in the EMBL, GenBank and DDBJ Nucleotide **Sequence** Databases under the accession number X77395.

8/7/3 (Item 3 from file: 5)
DIALOG(R)File 5:BIOSIS PREVIEWS(R)

09542647 BIOSIS NO.: 199497551017
Metabolic studies on Saccharomyces cerevisiae containing fused **citrate synthase**/malate dehydrogenase.
AUTHOR: Lindbladh Christer; Brodeur Richard D; Lilius G; Bulow Leif; Mosbach Klaus; Srere Paul A(a)
AUTHOR ADDRESS: (a)Pre-Clin. Sci. Unit, Dep. Veterans Aff. Med. Cent., 4500 S. Lancaster Rd., Dallas, TX 75216**USA
JOURNAL: Biochemistry 33 (39):p11684-11691 1994
ISSN: 0006-2960

DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: We have constructed two different fusion proteins consisting of the C-terminal end of CS1 fused in-frame to the N-terminal end of MDH1 and HSA, respectively. The fusion proteins were expressed in mutants of Saccharomyces cerevisiae in which CS1 and MDH1 had been deleted and the phenotypes of the transformants characterized. The results show that the fusion proteins are transported into the mitochondria and that they restore the ability for the yeast mutants CS1-, MDH1-, and CS1-/MDH1- to grow on acetate. Determination of CS1 activity in isolated mitochondria showed a 10-fold increase for the strain that expressed native CS1, relative to the parental. In the transformant with CS1/MDH1 fusion protein, parental levels of CS1 were observed, while one-fifth this amount was observed for the strain expressing the CS1/HSA conjugate. Oxygen consumption studies on isolated mitochondria did not show any significant differences between parental-type yeast and the strains expressing the different fusion proteins or native CS1. (3-13C)Propionate was used to study the Krebs TCA cycle metabolism of yeast cells containing CS1/MDH1 fusion constructs. The 13C NMR study was performed in respiratory-competent parental yeast cells and using the **genetically** engineered yeast cells consisting of CS1- mutants expressing native CS1 and the fusion proteins CS1/MDH1 and CS1/HSA, respectively. (3-13C)Propionate is believed to be metabolized to (2-13C)succinyl-CoA before it enters the TCA cycle in the mitochondria. This metabolite is then oxidized through two symmetrical intermediates, succinate and fumarate, followed by conversion to malate, oxalacetate, and other metabolites such as alanine. If the symmetrical intermediates randomly diffuse between the enzymes in the mitochondria, the 13C label should be equally distributed on the C2 and C3 positions of malate and alanine. However, if succinate and fumarate are directly transferred with conserved orientation between the active sites of the enzymes succinate thiokinase, succinate dehydrogenase, and fumarase, the labeling of the C2 and C3 positions of malate, oxalacetate, and alanine will be a symmetrical. During oxidation of (3-13C) propionate in parental cells, we observed an asymmetric labeling of the C2 and C3 positions of alanine where the 13C enrichment was significantly higher in the C3 position (C3/C2 = 14.3). Inhibition of succinate dehydrogenase with increasing amounts of malonate resulted in a concentration-dependent decrease in the asymmetric labeling of alanine. When(3-13C)propionate oxidation was performed in the CS1- yeast cells containing CS1, CS1/MDH1, and CS1/HSA, the CS/HSA transformant displayed significantly decreased asymmetry in the labeling of the C2 and C3 positions of alanine (C3/C2 = 2.9). No significant difference was found between parental cells and the CS1 and CS1/MDH1 transformants. Growth experiments on rich medium did not show any differences between the transformants. On minimal medium, however, the CS1/HSA transformant displayed an increased doubling time. These data show that, in yeast cells containing the CS1/MDH1 fusion protein, symmetrical intermediates are transferred directly from TCA cycle enzyme to TCA cycle enzyme under in vivo conditions just as is observed in the parental cell. The data also show that it is possible to alter this effect in the TCA cycle pathway by introduction of a **genetically** engineered CS1/HSA fusion protein. We also discuss these data in the context of the metabolon hypothesis for the Krebs TCA cycle.

8/7/4 (Item 4 from file: 5)
DIALOG(R)File 5:BIOSIS PREVIEWS(R)

09542563 BIOSIS NO.: 199497550933
Preparation and kinetic characterization of a fusion protein of yeast mitochondrial **citrate synthase** and malate dehydrogenase.
AUTHOR: Lindbladh C; Rault M; Hagglund C; Small W C; Mosbach K; Bulow L; Evans C; Srere P A(a)

AUTHOR ADDRESS: (a)Res. Serv., Dep. Veterans Aff. Med. Cent., 4500 S. Lancaster Rd., Dallas, TX 75216**USA
JOURNAL: Biochemistry 33 (39):p11692-11698 1994
ISSN: 0006-2960
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: We have expressed the **DNA** of the fusion of CS1 to MDH1 in Escherichia coli gltA-. The fusion protein (CS1/MDH1) is the C-terminus of CS1 linked in-frame to the N-terminus of MDH1 with a short linker of glycyl-seryl-glycyl. The fusion protein produced was isolated and purified. Gel filtration studies indicated that CS1/MDH1 had a M-r of apprx 170 000. Western blotting analysis with SDS gel indicated a M-r, of apprx 90 000-95 000 (theoretical M-r = 87 000). This is the expected M-r for the fusion protein subunit. The kinetics of CS1 and MDH1 activities of the fusion protein were compared to those of the free enzymes. In addition, the effect of AAT reaction, as a competitor for the intermediate OAA of the coupled MDH-CS reaction, was examined. It was observed that AAT was a less effective competitor for OAA when the CS1/MDH1 fusion protein is used than when the separate enzymes are employed. In addition, the transient time for the coupled reaction **sequence** was less for the fusion protein than for the free enzymes.

8/7/5 (Item 5 from file: 5)
DIALOG(R)File 5:BIOSIS PREVIEWS(R)

09427531 BIOSIS NO.: 199497435901
Origin and symbiotic role of a pSYM plasmid-**encoded citrate synthase gene** in Rhizobium tropici.
BOOK TITLE: Current **Plant** Science and Biotechnology in Agriculture; New horizons in nitrogen fixation
AUTHOR: Pardo M A; Hernendez-Lucas I; Martinez E
BOOK AUTHOR/EDITOR: Palacios R; Mora J; Newton W E: Eds
AUTHOR ADDRESS: Dep. Molecular Genetics, Centro Investigacion Sobre Fijacion Nitrogeno, Univ. Nacional Autonoma Mex.**Mexico
JOURNAL: Current Plant Science and Biotechnology in Agriculture 17p250 1993
BOOK PUBLISHER: Kluwer Academic Publishers, PO Box 989, 3300 AZ Dordrecht, Netherlands
Kluwer Academic Publishers, 101 Phillip Drive, Norwell, Massachusetts 02061, USA
CONFERENCE/MEETING: 9th International Congress on Nitrogen Fixation Cancun, Mexico December 6-12, 1992
ISSN: 0924-1949 ISBN: 0-7923-2207-X
RECORD TYPE: Citation
LANGUAGE: English

8/7/6 (Item 6 from file: 5)
DIALOG(R)File 5:BIOSIS PREVIEWS(R)

09424014 BIOSIS NO.: 199497432384
S. cerevisiae: An economical genome?
AUTHOR: Becam A-M; Nasr F; Jia Y; Slonimski P P; Herbert C J
AUTHOR ADDRESS: Cent. Genetique Mol. CNRS, F-91198 Gif-sur-Yvette**France
JOURNAL: Cell Biology International 18 (5):p361 1994
CONFERENCE/MEETING: IVth European Cell Biology Congress Prague, Czech Republic June 26-July 1, 1994
ISSN: 1065-6995
RECORD TYPE: Citation
LANGUAGE: English

8/7/7 (Item 7 from file: 5)
DIALOG(R)File 5:BIOSIS PREVIEWS(R)

09395679 BIOSIS NO.: 199497404049
The HAP2,3,4 transcriptional activator is required for derepression of the yeast **citrate synthase gene**, CIT1.
AUTHOR: Rosenkrantz Mark(a); Kell Christine S; Pennell Elizabeth A; Devenish Lousie J
AUTHOR ADDRESS: (a)Dep. Microbiol. Immunol., Virginia Commonwealth Univ./Med. Coll. Virginia, Richmond, VA 23298-06**USA
JOURNAL: Molecular Microbiology 13 (1):p119-131 1994
ISSN: 0950-382X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The yeast nuclear **gene** CIT1 **encodes** mitochondrial **citrate synthase**, which catalyses the first and rate-limiting step of the tricarboxylic acid (TCA) cycle. Transcription of CIT1 is subject to glucose repression. Mutations in HAP2, HAP3 or HAP4 block derepression of a CIT1-lacZ **gene** fusion. The HAP2,3,4 transcriptional activator also activates nuclear **genes encoding** components of the mitochondrial electron transport chain, and thus it co-ordinates derepression of two major mitochondrial functions. Two **DNA sequences** resembling the consensus HAP2,3,4-binding site (ACCAATNA) are located at approximately -310 and -290, upstream of the CIT1 coding **sequence**. Deletion and mutation analysis indicates that the -290 element is critical for activation by HAP2,3,4. Glucose-repressed expression of CIT1 is largely independent of HAP2,3,4, is repressed by glutamate, and requires a **DNA sequence** between -367 and -348. Evidence is presented for a second HAP2,3,4-independent activation element located just upstream and overlapping the -290 HAP2,3,4 element.

8/7/8 (Item 8 from file: 5)
DIALOG(R)File 5:BIOSIS PREVIEWS(R)

09305427 BIOSIS NO.: 199497313797
Organization of the centromeric region of chromosome XIV in Saccharomyces cerevisiae.
AUTHOR: Lalo Dominique; Stettler Sophie; Mariotte Sylvie; Gendreau Emmanuel ; Thuriaux Pierre(a)
AUTHOR ADDRESS: (a)Serv. Biochimie Genetique Moleculaire, Dep. Biologie Cellulaire Moleculaire, Commissariat l'Ener**France
JOURNAL: Yeast 10 (4):p523-533 1994
ISSN: 0749-503X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: A 15.1 kb fragment of the yeast genome was allocated to the centromeric region of chromosome XIV by **genetic** mapping. It contained six bona fide **genes**, RPC34, FUN34, CIT1 (Suissa et al., 1984), RLP7, PET8 and MRP7 (Fearon and Mason, 1988) and two large open reading frames, DOM34 and TOM34. RPC34 and RLP7 define strictly essential functions, whereas CIT1, PET8 and MRP7 **encode** mitochondrial proteins. The PET8 product belongs to a family of mitochondrial carrier proteins. FUN34 **encodes** a putative transmembraneous protein that is non-essential as judged from the normal growth of the fun34::LUK18 (URA3) allele, even on respirable substrates. TOM34 codes for a putative RNA binding protein, and DOM34 defines a hypothetical polypeptide of 35 kDa, with no significant homology to known proteins. The region under study

also contains two divergently transcribed tDNAs, separated only by a chimeric transposable element. This tight tDNA linkage pattern is commonly encountered in yeast, and a **general** hypothesis is proposed for its emergence on the Saccharomyces cerevisiae genome. RPC34, RLP7, PET8 and MRP7 are unique on the yeast genome, but the remaining **genes** belong to an extant centromeric duplication between chromosome III and XIV. The **sequences** have been deposited in the EMBL/GenBank data libraries under Accession Numbers L11277, L19167, M11344, M22116, V02536, X00782 and X63746.

8/7/9 (Item 9 from file: 5)
DIALOG(R)File 5:BIOSIS PREVIEWS(R)

09181975 BIOSIS NO.: 199497190345
Distinct upstream activation regions for glucose-repressed and derepressed expression of the yeast **citrate synthase gene** CIT1.
AUTHOR: Rosenkrantz Mark(a); Kell Christine S; Pennell Elizabeth A; Webster Michelle; Devenish Louise J
AUTHOR ADDRESS: (a)Dep. Microbiol. Immunol., Virginia Commonwealth Univ., Med. College Virginia, Richmond, VA 23298**USA
JOURNAL: Current Genetics 25 (3):p185-195 1994
ISSN: 0172-8083
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The yeast CIT1 (mitochondrial **citrate synthase**) **gene** is subject to glucose repression and is further repressed by glucose plus glutamate. Based on deletion analysis of a CIT1-lacZ **gene** fusion, **DNA sequences** between -548 and -273 are required for full expression of CIT1. The region of transcription initiation and the putative TATA element are located at -150 to -100 and -195 respectively. A restriction fragment containing **DNA sequences** between -457 and -211 conferred activation and glucose-glutamate regulation when placed in either orientation upstream of a UAS-less heterologous yeast **gene**. Deletion of **DNA sequences** between -291 and -273 specifically eliminated derepression of CIT1, and destroyed one of two closely-spaced, potential binding sites for the HAP2,3,4 transcriptional activator protein. Ten-base-pair block substitutions in the region -367 to -348 reduced glucose-repressed expression. Thus, it appears that distinct **DNA sequences** upstream of CIT1 activate expression in glucose-repressed and derepressed cells. Possible mechanisms of regulation by glutamate plus glucose, are discussed.

8/7/10 (Item 10 from file: 5)
DIALOG(R)File 5:BIOSIS PREVIEWS(R)

09131865 BIOSIS NO.: 199497140235
Characterization of the cit-1 **gene** from Neurospora crassa **encoding** the mitochondrial form of **citrate synthase**.
AUTHOR: Ferea Tracy; Contreras Emeline T; Oung Thim; Bowman Emma J; Bowman Barry J(a)
AUTHOR ADDRESS: (a)Dep. Biol., Sinsheimer Lab., Univ. Calif., Santa Cruz, CA 95064**USA
JOURNAL: Molecular & General Genetics 242 (1):p105-110 1994
ISSN: 0026-8925
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: We have isolated the **cDNA** and corresponding genomic

DNA encoding citrate synthase in Neurospora crassa. Analysis of the protein coding region of this **gene**, named cit-1, indicates that it specifies the mitochondrial form of **citrate synthase**. The predicted protein has 469 amino acids and a molecular mass of 52 002 Da. The **gene** is interrupted by four introns. Hybridization experiments show that a cit-1 probe binds to two different fragments of genomic **DNA**, which are located on different chromosomes. Neurospora crassa may have two isoforms of **citrate synthase**, one in the mitochondria and the other in microbodies.

? t s9/pn,ab/all

9/PN,AB/1 (Item 1 from file: 654)
DIALOG(R)File 654:(c) FORMAT ONLY 1999 THE DIALOG CORP. All rts. reserv.

PATENT NO.: 6,008,436
ISSUED: December 28, 1999 (19991228)

ABSTRACT

Nematode-resistant **transgenic plants** are disclosed. The **plants** comprise **plant** cells containing a DNA construct comprising a transcription cassette, which construct comprises, in the 5' to 3' direction, a promoter operable in the **plant** cells, and a DNA comprising at least a portion of a DNA sequence encoding a nematode-inducible transmembrane pore protein in either the sense or **antisense** orientation. Intermediates for producing the same along with methods of making and using the same are also disclosed. In an alternate embodiment of the invention, the sense or **antisense** DNA is replaced with a DNA encoding an enzymatic RNA molecule directed against the mRNA transcript of a DNA sequence encoding a nematode-inducible transmembrane pore protein.

9/PN,AB/2 (Item 2 from file: 654)
DIALOG(R)File 654:(c) FORMAT ONLY 1999 THE DIALOG CORP. All rts. reserv.

PATENT NO.: 5,973,228
ISSUED: October 26, 1999 (19991026)

ABSTRACT

A cDNA molecule encoding coniferin beta-glucosidase is disclosed. This enzyme catalyzes one of the last steps in the synthesis of lignin in **plants**. **Plants** having modified lignin content may be produced by transformation with this cDNA (or parts of the cDNA), for example, in either sense or **antisense** orientation. The invention includes methods of altering-lignin content in **plants** using this cDNA, as well as **transformed plants**, such as conifers, having modified lignin content.

9/PN,AB/3 (Item 3 from file: 654)
DIALOG(R)File 654:(c) FORMAT ONLY 1999 THE DIALOG CORP. All rts. reserv.

PATENT NO.: 5,959,181
ISSUED: September 28, 1999 (19990928)

ABSTRACT

The present invention relates to a method of preparation of **transgenic plants** resistant to viral infections by introducing into the genoma of a host **plant** an **antisense** gene construct constituted by: the domain F of the subgenomic promoter of a viral RNA; a leader sequence of a viral ORF, downstream from said subgenomic promoter; the gene encoding a viral coat protein, downstream from said leader sequence; and the 3'-terminal region of a viral RNA, downstream from said gene. The present invention also relates to a recombinant vector comprising

a promoter functional in a host **plant**, and, operably linked to this promoter, the **antisense** gene construct of the present invention.

9/PN,AB/4 (Item 4 from file: 654)

PATENT NO.: 5,942,661
ISSUED: August 24, 1999 (19990824)

ABSTRACT

A method of inhibiting the production of mycotoxins of fungus, such as aflatoxin-producing and sterigmatocystin-producing fungi, in **plants** susceptible to contamination by such mycotoxins consists of introducing into the susceptible **plant** a gene encoding for lipoxygenase pathway enzyme of the mycotoxin. Exemplary of the lipoxygenase pathway enzymes are soybean lipoxygenase, allene oxidase, hydroperoxide lyase and hydroperoxide dehydratase. The resulting **transgenic plant** demonstrates substantial resistance to mycotoxin contamination of such fungus. **Plants** which are substantially resistant to mycotoxin contamination of Aspergillus spp. are further obtained by incorporating into mycotoxin susceptible **plant antisense** genes for the 9-hydroperoxide fatty acid producing lipoxygenases.

9/PN,AB/5 (Item 5 from file: 654)

PATENT NO.: 5,929,303
ISSUED: July 27, 1999 (19990727)

ABSTRACT

Expansins are proteins that induce extension in isolated **plant** cell walls in vitro and have been proposed to disrupt non-covalent interactions between hemicellulose and cellulose microfibrils. Because the **plant** primary cell wall acts as a constraint to cell enlargement, this process may be integral to **plant** cell expansion and studies of expansins have focused on their role in growth. We have discovered an expansin (Ex1) from tomato, melon and strawberry that is highly abundant and specifically expressed in ripening fruit, a developmental period when growth has ceased but when selective disassembly of cell wall components is pronounced. Also disclosed are expression vectors containing the Ex1 coding sequence, expression vectors containing an Ex1 sequence in the **antisense** orientation, Ex1 proteins, and **transgenic plants** which express both sense and **antisense** exogenous Ex1.

9/PN,AB/6 (Item 6 from file: 654)

PATENT NO.: 5,925,807
ISSUED: July 20, 1999 (19990720)

ABSTRACT

The invention relates to the DNA and protein encoded by the GA4 locus. This protein is believed to be a member of the family of enzymes involved in the biosynthesis of the gibberellin family (GA) of **plant** growth hormones which promote various growth and developmental processes in higher **plants** , such as seed germination, stem elongation, flowering and fruiting. More specifically, the protein encoded by the GA4 locus is an hydroxylase. The invention also relates to vectors containing the DNA and the expression of the protein encoded by the DNA of the invention in a host cell. Additional aspects of the invention are drawn to host cells

transformed with the DNA or **antisense** sequence of the invention, the use of such host cells for the maintenance, or expression or inhibition of expression of the DNA of the invention and to **transgenic plants** containing DNA of the invention. Finally, the invention also relates to the use of the protein encoded by the GA4 locus to alter aspects of **plant** growth.

9/PN,AB/7 (Item 7 from file: 654)
DIALOG(R)File 654:(c) FORMAT ONLY 1999 THE DIALOG CORP. All rts. reserv.

PATENT NO.: 5,919,998
ISSUED: July 06, 1999 (19990706)

ABSTRACT

Plant growth and **plant** growth habit can be controlled without the application of exogenous **plant** hormones or hormone mimetics using the nucleic acid sequences and methods provided. UDP-Glucose: Indol-3-ylacetyl-glucosyl transferase (IAGlu Transferase) amino acid sequence and nucleic acid coding sequences for this enzyme, specifically exemplified for Zea mays, are provided. Nucleic acid constructs directing the expression of IAGlu Transferase and the expression of **antisense** RNA specific therefor allows the control of growth habit and **plant** size in **transgenic plants** containing such nucleic acid constructs.

9/PN,AB/8 (Item 8 from file: 654)
DIALOG(R)File 654:(c) FORMAT ONLY 1999 THE DIALOG CORP. All rts. reserv.

PATENT NO.: 5,908,973
ISSUED: June 01, 1999 (19990601)

ABSTRACT

DNA constructs comprising DNA sequences encoding fruit-ripening-related proteins may be **transformed** into **plants** to modify **plant** characteristics (particularly fruit quality). New DNA sequences are disclosed; cDNA and genomic clones have been deposited; new fruit-ripening-related promoter sequences may also be obtained. Sense and **antisense** constructs for **plant** transformation are described. Genetically modified **plants** may be used to produce improved fruit and may also be used in breeding programs to produce hybrid seed.

9/PN,AB/9 (Item 9 from file: 654)
DIALOG(R)File 654:(c) FORMAT ONLY 1999 THE DIALOG CORP. All rts. reserv.

PATENT NO.: 5,883,076
ISSUED: March 16, 1999 (19990316)

ABSTRACT

Systemin, an 18 amino acid peptide hormone and first polypeptide hormone found in **plants**, induces expression of defense genes in **plants** wounded mechanically or by predators including herbivores, insects, bacteria and viruses. The precursor for systemin is encoded as a 200 amino acid prosystemin molecule that has the systemin peptide sequence located near the carboxyl-terminus. Both a 951 bp cDNA for prosystemin and 4526 bp genomic DNA were cloned and the organization of the gene was determined. **Transgenic plants** constructed with **antisense** prosystemin DNA fail to mount a defensive response to wounding. **Transgenic plants** constructed with increased copy number of prosystemin genes exhibit increased resistance to wounding. Insect larval that feed on **transgenic plants** constructed with increased copy number of

prosystemin genes exhibit decreased growth weight compared to larval that feed on wild type **plants**. A tomato systemin polypeptide has an amino acid sequence NH sub 3 -AVQSKPPSKRDPPKMQTD-COO-.

9/PN,AB/10 (Item 10 from file: 654)
DIALOG(R)File 654:(c) FORMAT ONLY 1999 THE DIALOG CORP. All rts. reserv.

PATENT NO.: 5,876,964
ISSUED: March 02, 1999 (19990302)

ABSTRACT

A cDNA encoding geranyl diphosphate synthase from peppermint has been isolated and sequenced, and the corresponding amino acid sequence has been determined. Accordingly, an isolated DNA sequence (SEQ ID No:1) is provided which codes for the expression of geranyl diphosphate synthase (SEQ ID No:2) from peppermint (Mentha piperita). In other aspects, replicable recombinant cloning vehicles are provided which code for geranyl diphosphate synthase or for a base sequence sufficiently complementary to at least a portion of the geranyl diphosphate synthase DNA or RNA to enable hybridization therewith (e.g., **antisense** geranyl diphosphate synthase RNA or fragments of complementary geranyl diphosphate synthase DNA which are useful as polymerase chain reaction primers or as probes for geranyl diphosphate synthase or related genes). In yet other aspects, modified host cells are provided that have been **transformed**, transfected, infected and/or injected with a recombinant cloning vehicle and/or DNA sequence encoding geranyl diphosphate synthase. Thus, systems and methods are provided for the recombinant expression of geranyl diphosphate synthase that may be used to facilitate the production, isolation and purification of significant quantities of recombinant geranyl diphosphate synthase for subsequent use, to obtain expression or enhanced expression of geranyl diphosphate synthase in **plants** in order to enhance the production of monoterpenoids, to produce geranyl diphosphate in cancerous cells as a precursor to monoterpenoids having anti-cancer properties or may be otherwise employed for the regulation or expression of geranyl diphosphate synthase or the production of geranyl diphosphate.

9/PN,AB/11 (Item 11 from file: 654)
DIALOG(R)File 654:(c) FORMAT ONLY 1999 THE DIALOG CORP. All rts. reserv.

PATENT NO.: 5,874,269
ISSUED: February 23, 1999 (19990223)

ABSTRACT

The invention provides purified proteins, DNA sequences that code on expression therefore and recombinant DNA molecules, including hosts **transformed** therewith for transforming coffee **plants** to suppress the expression of enzymes necessary for ethylene synthesis. The DNA sequences and recombinant DNA molecules are characerized in that they code on expression for the enzymes ACC synthase or ACC oxidase that are elements of the pathway for ethylene biosynthesis in coffee **plants**. Coffee **plants** are **transformed** with vectors containing ACC synthase and/or with ACC oxidase DNA sequences that code on expression for the respective mRNA that is **antisense** to the mRNA for ACC synthase and/or ACC oxidase. The resulting **antisense** mRNA binds to the respective ACC synthase and/or ACC oxidase mRNA, thereby inactivating the mRNA encoding one or more enzymes in the pathway for ethylene synthesis. The described DNA sequences can also be used to block synthesis of ACC synthase or ACC oxidase using co-suppression. The result in either event is that the **transformed plants** are incapable of synthesizing ethylne, though other aspects of their metabolism is not affected.

9/PN,AB/12 (Item 12 from file: 654)
DIALOG(R)File 654:(c) FORMAT ONLY 1999 THE DIALOG CORP. All rts. reserv.

PATENT NO.: 5,871,988
ISSUED: February 16, 1999 (19990216)

ABSTRACT

cDNA encoding (-)-4S-limonene synthase from spearmint has been isolated and sequenced, and the corresponding amino acid sequence has been determined. Accordingly, isolated DNA sequences are provided which code for the expression of limonene synthase, such as the sequence designated SEQ ID No:11 which encodes limonene synthase from spearmint (Mentha spicata). In other aspects, replicable recombinant cloning vehicles are provided which code for limonene synthase or for a base sequence sufficiently complementary to at least a portion of the limonene synthase DNA or RNA to enable hybridization therewith (e.g., **antisense** limonene synthase RNA or fragments of complementary limonene synthase DNA which are useful as polymerase chain reaction primers or as probes for limonene synthase or related genes). In yet other aspects, modified host cells are provided that have been **transformed**, transfected, infected and/or injected with a recombinant cloning vehicle and/or DNA sequence encoding limonene synthase. Thus, systems and methods are provided for the recombinant expression of limonene synthase that may be used to facilitate the production, isolation and purification of significant quantities of recombinant limonene synthase (or of the primary enzyme product, limonene) for subsequent use, to obtain expression or enhanced expression of limonene synthase in **plants** to attain enhanced limonene production as a predator defense mechanism, or may be otherwise employed for the regulation or expression of limonene synthase or the production of limonene.

9/PN,AB/13 (Item 13 from file: 654)
DIALOG(R)File 654:(c) FORMAT ONLY 1999 THE DIALOG CORP. All rts. reserv.

PATENT NO.: 5,866,780
ISSUED: February 02, 1999 (19990202)

ABSTRACT

The present invention provides the nucleotide structure and organization of a novel maize chlorotic dwarf virus genome designated MCDV-Tn. Methods for using the complete or partial MCDV-Tn genomic sequence as a probe for diagnostic and other purposes are taught. Methods for inhibiting MCDV-Tn infection are also taught. These methods include the generation of **transformed plants** capable of expressing MCDV-Tn proteins, either in modified or unmodified form, and **antisense** sequences targeting MCDV-Tn genomic RNA. Recombinant production of MCDV-Tn proteins in appropriate host cells is also taught.

9/PN,AB/14 (Item 14 from file: 654)
DIALOG(R)File 654:(c) FORMAT ONLY 1999 THE DIALOG CORP. All rts. reserv.

PATENT NO.: 5,846,821
ISSUED: December 08, 1998 (19981208)

ABSTRACT

Isolated nucleic acid molecules encoding novel members of the MRT family of polypeptides which include, in a preferred embodiment, at least one transmembrane domain having at least about 30%, more preferably at least about 50%, 55%, 60%, 70%, 80% or 90% amino acid sequence identity with SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8 or SEQ ID NO:14 and/or at least one histidine rich domain, are described. The MRT polypeptides of the invention are capable of transporting metals such as Fe(II), Cd, Co, Mn,

Pb, Hg and Zn. **Transgenic plants** in which expression of an MRT polypeptide of the invention is altered are also described. These **transgenic plants** can be used to remove pollutants from soil or as nutritional supplements to treat iron- or zinc-deficiency. **Antisense** nucleic acid molecules, recombinant expression vectors containing nucleic acid molecules of the invention, and host cells into which the expression vectors have been introduced are also described. The invention further provides isolated MRT polypeptides, fusion polypeptides and active fragments thereof. Therapeutic methods utilizing compositions of the invention are also provided.

9/PN,AB/15 (Item 15 from file: 654)

PATENT NO.: 5,844,121
ISSUED: December 01, 1998 (19981201)

ABSTRACT

A method of inhibiting the production of mycotoxins of fungus, such as aflatoxin-producing and sterigmatocystin-producing fungi, in **plants** susceptible to contamination by such mycotoxins consists of introducing into the susceptible **plant** a gene encoding for lipoxygenase pathway enzyme of the mycotoxin. Exemplary of the lipoxygenase pathway enzymes are soybean lipoxygenase, allene oxidase, hydroperoxide lyase and hydroperoxide dehydratase. The resulting **transgenic plant** demonstrates substantial resistance to mycotoxin contamination of such fungus. **Plants** which are substantially resistant to mycotoxin contamination of Aspergillus spp. are further obtained by incorporating into mycotoxin susceptible **plant antisense** genes for the 9-hydroperoxide fatty acid producing lipoxygenases.

9/PN,AB/16 (Item 16 from file: 654)

PATENT NO.: 5,834,265
ISSUED: November 10, 1998 (19981110)

ABSTRACT

A multifunctional RNA having self-processing activity, the preparation thereof and the use thereof Host cells can be **transformed** so that they express ribozyme RNA and **antisense** RNA which are connected with each other via a spacer. The RNA molecules can, for example, be complementary to a certain viral RNA. **Plants** which have been **transformed** with genes coding for RNA of this type show a significantly improved resistance to viruses.

9/PN,AB/17 (Item 17 from file: 654)

PATENT NO.: 5,830,724
ISSUED: November 03, 1998 (19981103)

ABSTRACT

A process is provided whereby the constitution of starch produced in a **plant** is altered without there being a substantial change in the total amount of starch which is produced. In the process a **plant** cell is **transformed** using a chimaeric gene comprising an **antisense** coding sequence from the waxy locus of a **plant** genome or an **antisense** similar coding sequence from a non-**plant** genome.

9/PN,AB/18 (Item 18 from file: 654)

PATENT NO.: 5,821,052
ISSUED: October 13, 1998 (19981013)

ABSTRACT

The inhibition of proteins synthesis by an **antisense** RNA-tRNA complex which is capable of inhibiting translation is described. Under certain conditions, growth of organisms is inhibited by inhibition of non-specific translation by an **antisense** RNA construct to a tRNA target. In vitro, cell-free inhibition of viral protein translation is described. **Transformed** microorganisms are disclosed. The invention has applicability in the control of cell growth, such as viruses, bacteria, infected cells, or tumor cells. The invention is useful in animal and **plant** fields.

9/PN,AB/19 (Item 19 from file: 654)

PATENT NO.: 5,744,693
ISSUED: April 28, 1998 (19980428)

ABSTRACT

The invention includes **plants** having at least one cell **transformed** with a vector comprising at least a portion of an agamous nucleic acid. Such **plants** have a phenotype characterized by altered floral development such as an AG or AP2 phenotype. The invention also includes vectors comprising at least a portion of an agamous nucleic acid operably linked to a promoter other than the promoter naturally associated with the agamous nucleic acid. In an alternate embodiment, the vector comprises at least a portion of an agamous nucleic acid operably linked in an **antisense** orientation to a promoter. The invention also includes methods using such vectors for producing **plants** having altered floral development.

9/PN,AB/20 (Item 20 from file: 654)

PATENT NO.: 5,707,840
ISSUED: January 13, 1998 (19980113)

ABSTRACT

A multifunctional RNA having self-processing activity, the preparation thereof and the use thereof.

Host cells can be **transformed** so that they express ribozyme RNA and **antisense** RNA which are connected with each other via a spacer. The RNA molecules can, for example, be complementary to a certain viral RNA. **Plants** which have been **transformed** with genes coding for RNA of this type show a significantly improved resistance to viruses.

9/PN,AB/21 (Item 21 from file: 654)

PATENT NO.: 5,670,454
ISSUED: September 23, 1997 (19970923)

ABSTRACT

Use of herbicides of the auxin type for controlling broad-leaved weeds and grass weeds in **transgenic** crop **plants** which contain an ACC synthase **antisense** gene, ACC oxidase gene, ACC deaminase gene or combinations thereof is described.

9/PN,AB/22 (Item 22 from file: 654)
DIALOG(R)File 654:(c) FORMAT ONLY 1999 THE DIALOG CORP. All rts. reserv.

PATENT NO.: 5,659,121
ISSUED: August 19, 1997 (19970819)

ABSTRACT

DNA constructs comprise a DNA sequence homologous to some or all of the pectinesterase gene encoded by the clone pB8 (Sequence ID No.1), under control of a transcriptional initiation region operative in **plants** for transcribing this DNA sequence, optionally in the **antisense** direction to produce RNA complementary to the gene mRNA. From such constructs may be derived **transformed plant** cells and **plants** in which expression of pectinesterase genes is inhibited: fruit from the **plants** (such as tomatoes) can show modified ripening properties.

9/PN,AB/23 (Item 23 from file: 654)
DIALOG(R)File 654:(c) FORMAT ONLY 1999 THE DIALOG CORP. All rts. reserv.

PATENT NO.: 5,597,718
ISSUED: January 28, 1997 (19970128)

ABSTRACT

A method is disclosed which describes the identification of cDNA clones useful for identifying fiber genes in cotton. The cDNA clones are useful in developing corresponding genomic clones from fiber producing **plants** to enable genetic engineering of cotton and other **plants** using these genes. The fiber-specific genes are identified by differential cDNA library screenings. Coding sequences from these isolated genes are used in sense or **antisense** orientation to alter the fiber characteristics of **transgenic** fiber-producing **plants**.

9/PN,AB/24 (Item 24 from file: 654)
DIALOG(R)File 654:(c) FORMAT ONLY 1999 THE DIALOG CORP. All rts. reserv.

PATENT NO.: 5,569,831
ISSUED: October 29, 1996 (19961029)

ABSTRACT

Methods of creating **transgenic** tomatoes containing a lowered level of polygalacturonase isoform 1 are disclosed. The isolation of a DNA sequence encoding the polygalacturonase beta-subunit is disclosed. The beta-subunit sequence can be used to construct both sense and **antisense** **plant** expression constructions which can be **transformed** into tomato **plants**. The **transgenic** tomato **plants** have altered levels of polygalacturonase isoforms in that the level of isoform 1 is dramatically reduced. The resulting tomato fruit has a polygalacturonase activity level that is more heat labile, and thus more convenient for processing, and an increased level of soluble pectins.

9/PN,AB/25 (Item 25 from file: 654)
DIALOG(R)File 654:(c) FORMAT ONLY 1999 THE DIALOG CORP. All rts. reserv.

PATENT NO.: 5,569,829
ISSUED: October 29, 1996 (19961029)

ABSTRACT

A method is provided for making fruit (particularly tomatoes) having increased solids content which comprises cultivating fruit-bearing **plants** in which expression of genes homologous to pTOM36 is at least partially inhibited. For this purpose the fruit may be **transformed** with DNA constructs comprising a DNA sequence homologous to some or all of the gene encoded by the clone pTOM36. The clone is adapted to generate sense or **antisense** RNA under control of a **plant** promoter.

9/PN,AB/26 (Item 26 from file: 654)
DIALOG(R)File 654:(c) FORMAT ONLY 1999 THE DIALOG CORP. All rts. reserv.

PATENT NO.: 5,545,815
ISSUED: August 13, 1996 (19960813)

ABSTRACT

The present invention provides novel **transgenic plants** comprising **antisense** DNA constructs which inhibit expression of ethylene perception genes. The **plants** exhibit decreased levels of ethylene-mediated responses, such as fruit ripening.

9/PN,AB/27 (Item 27 from file: 654)
DIALOG(R)File 654:(c) FORMAT ONLY 1999 THE DIALOG CORP. All rts. reserv.

PATENT NO.: 5,498,533
ISSUED: March 12, 1996 (19960312)

ABSTRACT

A method of controlling growth and development of **plants** is provided herein. More particularly, a method of controlling growth and development of potato **plants** by increasing or decreasing the expression of a gene encoding calmodulin is set forth. **Transgenic** potato **plants** carrying sense nucleic acid constructs of pPCM-1, a cDNA clone of potato calmodulin, exhibit unexpected increased shoot and tuber growth, whereas **plants** carrying **antisense** nucleic acid constructs exhibit decreased shoot and tuber growth.

9/PN,AB/28 (Item 28 from file: 654)
DIALOG(R)File 654:(c) FORMAT ONLY 1999 THE DIALOG CORP. All rts. reserv.

PATENT NO.: 5,378,819
ISSUED: January 03, 1995 (19950103)

ABSTRACT

Systemin is an 18 amino acid peptide hormone that induces expression of defense genes in **plants** wounded mechanically or by predators including herbivores, insects, bacteria and viruses. The precursor for systemin is encoded as a 200 amino acid prosystemin molecule that has the systemin peptide sequence located near the carboxy-terminus. Both a 951 bp cDNA for prosystemin and 4526 bp genomic DNA were cloned and the organization of the gene was determined. **Transgenic plants** constructed with **antisense** prosystemin DNA fail to mount a defensive response to wounding. **Transgenic plants** constructed with increased copy number of prosystemin genes exhibit increase resistance to wounding. A tomato systemin polypeptide has an amino acid sequence NH sub 3

--AVQSKPPSKRDPPKMQTD--COO--.

9/PN,AB/29 (Item 29 from file: 654)
DIALOG(R)File 654:(c) FORMAT ONLY 1999 THE DIALOG CORP. All rts. reserv.

PATENT NO.: 5,365,016
ISSUED: November 15, 1994 (19941115)

ABSTRACT

A process is provided whereby the constitution of starch produced in a **plant** is altered without there being a substantial change in the total amount of starch which is produced. In the process a **plant** cell is **transformed** using a chimaeric gene comprising an **antisense** coding sequence from the waxy locus of a **plant** genome or an **antisense** similar coding sequence from a non-**plant** genome.

9/PN,AB/30 (Item 30 from file: 654)
DIALOG(R)File 654:(c) FORMAT ONLY 1999 THE DIALOG CORP. All rts. reserv.

PATENT NO.: 5,254,800
ISSUED: October 19, 1993 (19931019)

ABSTRACT

DNA constructs comprise a DNA sequence homologous to some or all of the gene encoded by the clone pTOM36. The constructs may further comprise a transcriptional initiation region operative in **plants** for transcribing this DNA sequence, optionally in the **antisense** direction to produce mRNA complementary to the pTOM36 gene. **Transformed** **plant** cells and **plants** may be derived from such constructs: fruit from the **plants** (such as tomatoes) are expected to have modified ripening properties.
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Set	Items	Description
S1	0	CITRATE? (1A) (SYNTHETASE? OR SYNTHASE?)
S2	72	CITRATE? (1N) (SYNTHETASE? OR SYNTHASE?)
S3	6678	ANTISENSE?
S4	1	S2 AND S3
S5	2287	(TRANSGENIC? OR TRANSFORMED) (5N) (PLANT OR PLANTS)
S6	1010	S5 AND S3
S7	633	((TRANSGENIC? OR TRANSFORMED) AND (PLANT OR PLANTS))/AB
S8	603	ANTISENSE/AB
S9	30	S7 AND S8
S10	86814	ENZYM?